

Figure 1

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Figure 2

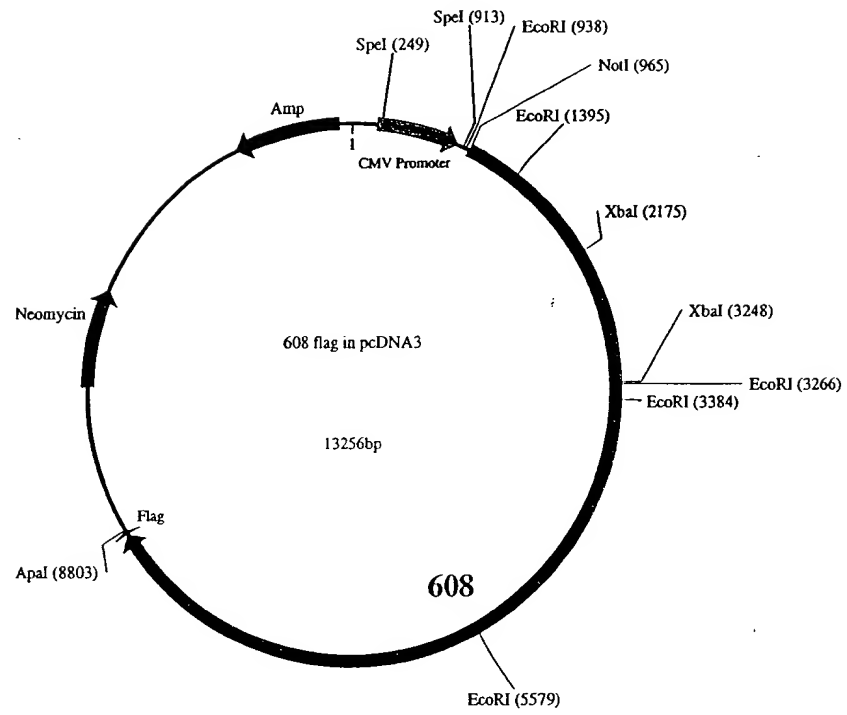


Figure 3

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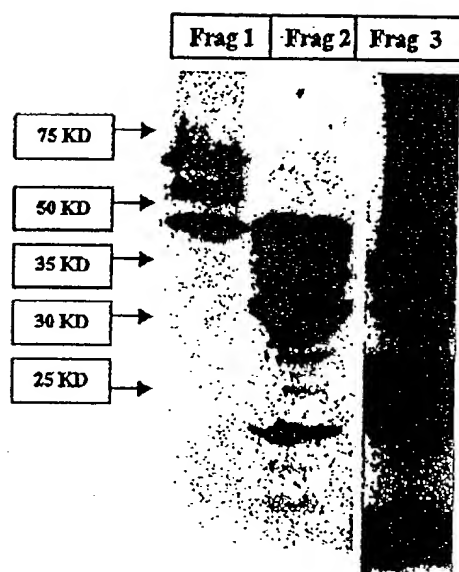
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Figure 4



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Figure 5

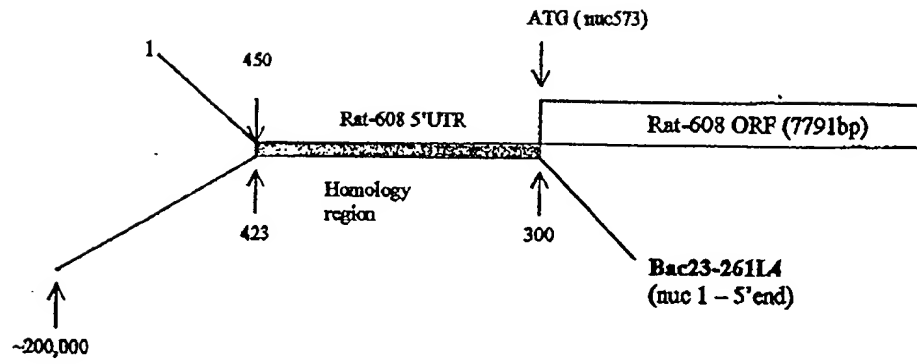


Figure 6

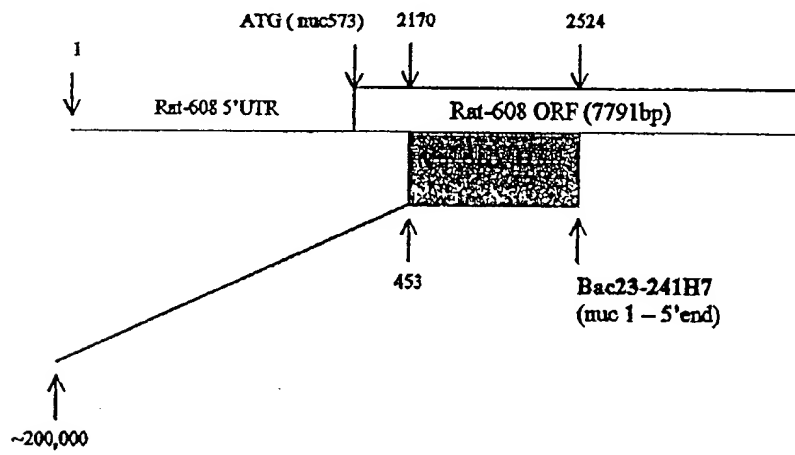


Figure 7

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Nuc 8218

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TGTAAGAGTTTTTACACACCCGAAGTGGGAAACTTAAAGGATTAGACAAGTCTAACAAATGAG
AATGGGAGAAACAAAAGAGACTGCACAGGGAGCCCTTCTCTGCTTATAATCTTGACAC
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ATAATAGCAATCAAAGCAATAACACCCACTGTTTACAGAGACTTTAAACATGAAACTGGG
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GGTCAAAAACAGAAAATATGTAAAAAGTTATTGTTTATTAGTATTTCATGTTCTTTCTT
TTTTAAAAATGTTATGCTTAGAACTAATTAAGATTAGATTAGATTAGATTAGAAAATAAT
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Exon 4 ? (Nuc 11286) ↓

TTGTGAAAGTTCTTTGAGAAAAACAAATATGCCATATCTTTCTTACAGGCTTAAAAATG
AGCTATAACAAAGTCCAAATAATTGAGAAGGATACTTTGTATGGACTCAGGAGCTTGACCCGG
TTGCCAOCCTGGATCACAACCAATTGAGTTTATCAACCCCGAGGCGTTTAAOGGACTCACCTTGC
TCCGCTTGGTACATCTAGAAGGAAAACCGGCTGACAAAGCTCCATCCAGACACATTTGTCTCTTT
GAGCTATCTOCAGATATTTAAAACTCCTTCATTAAGNAOCTGTACTTGTATGATAACTTCATG
ACCTCCTCCCAAAGAAATGGTCTCTCTATGCCAAAOCTAGAAAGCCTTTACTTGCATGGAA
ACCCATGGAOCCTGTGACTGCATTTAAAGTGTTGTCCGAGTGGATGCAGGGAAACCCAGGTA

Nuc 11680 ↑

ACTATCTGTGTTGTTGTTTCTTTTATARKAOGTATTTCTCAATTTCAATTTAGAATGA
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CCTGGCATTCCCTGTACTGGGCGCATATAAAGTTTGGGTGTCCAAATGGACCTCTCTTCC
AGTGATGGCCAACTAGGCCATCTTTTGATACATATGCAGCTAGAGTCAAGAGCTCTGGGG
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Nuc 11967 ↑

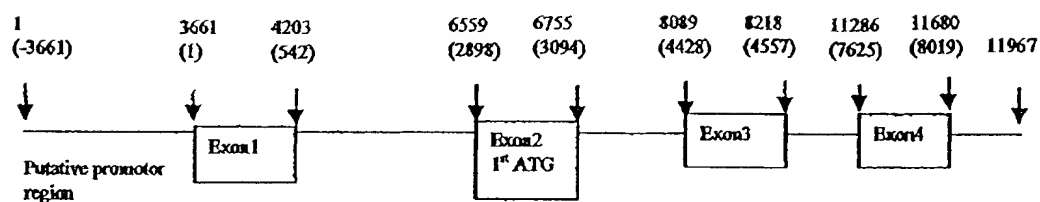
(SEQ ID NO:3)

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Figure 8

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length
1	1	542	542	2356
2	2898	3094	197	1334
3	4428	4557	130	3068
4	7625	8019	394	

Figure 9



[illegible]

cDNA_rat genomic_hu	1	1	ogagagacgacagaagggttacggctgcgagaagacgacagaaggggtccag
cDNA_rat genomic_hu	51	1	aaaaaggaaagtgcctggaggggagtggggacaaaagcagcagacgaagtga
cDNA_rat genomic_hu	101	1	atgtcacttcagtgactgaggccaggcaaaaogcgcggaaggattttgt
cDNA_rat genomic_hu	151	1	gtagccttgggaocctttcatagacactgatgacacgtttacgaaaaatag
cDNA_rat genomic_hu	201	1	aaattttgaggagaaaogcctgggccttcggaaggagtgattgattagta
cDNA_rat genomic_hu	251	1	cttgcaagtttagtgactttaaggagaactaactaatgtatactattga
cDNA_rat genomic_hu	301	1	gggaggaggagagagcattacagagtttcagcagcagcaggaaagccttg
cDNA_rat genomic_hu	351	1	gttaatttggaaatggatgatagcattaaataacagaagcgctccagg
cDNA_rat genomic_hu	401	1	tctctgaagottcagctcccccagctgaaagccagaaaagactaagccaac
cDNA_rat genomic_hu	451	1	taagoccttttgatccctttggaagcaaaagaactttccttcctcgggtga
cDNA_rat genomic_hu	501	1	agactctcctcagaaagatttcctgtctctgcctatgttacaagaggaaac
cDNA_rat genomic_hu	551	1	aaaaccaagacagaagagctcaggatgcagggtgagaggcagggaagtcag
cDNA_rat genomic_hu	601	1	oggtttgttgatctccctcaactgctgtctgcctgggtggtcaocctggga
cDNA_rat genomic_hu	651	1	gcagggcctgtcctgcgcctgtgctgtctatgtgccacagaggtgcac
cDNA_rat genomic_hu	701	1	tgtacatttcggtaacctgaacctccatcccagatgggaatcccgccaatgt
cDNA_rat genomic_hu	751	1	ggaacgaataaatttaggatataacagccttactagattgacagaaaacg
cDNA_rat genomic_hu	801	1	actttgatggcctgagcaaaactggagttactcatgotgcaagtaatggc
cDNA_rat genomic_hu	851	1	attcacagagtcagtgacaagaccttctcgggcttgagtccttgaggt
cDNA_rat genomic_hu	901	1	cttaaaaatgagctatacaaaagtcocaaatcattoggaaggatactttct

cDNA_rat	951	acggactcgggagcttggtcgggttgacactggatcacacaacattgaa
genomic_hu	1	-----
cDNA_rat	1001	ttcatcaacctgagggccttttatggacttacctogctccgcttggtaca
genomic_hu	1	-----
cDNA_rat	1051	tttagaaggaaacccggtcacaagctccatccagacacatttgtotcat
genomic_hu	1	-----
cDNA_rat	1101	taagotatctccagatatttaaacctctttcattaagtacactgttcttg
genomic_hu	1	-----
cDNA_rat	1151	tctgataacttcctgacctccctcccaaaagaaatggtctootaatgcc
genomic_hu	1	-----
cDNA_rat	1201	aaacotagaaagcctgtatttgcattgaaacccatggacctgtgactgcc
genomic_hu	1	-----
cDNA_rat	1251	atttaaagtgggtgtotgagtgatgcagggaacccatataataaaa
genomic_hu	1	-----
cDNA_rat	1301	tgcaagaaagacagaagotcttcagtcctcagcaatgtccctttgcat
genomic_hu	1	-----
cDNA_rat	1351	gaacccagggatctctaaaggcagaccctttgctatggtacocatgtggag
genomic_hu	1	-----
cDNA_rat	1401	ctttcctatgtacaaagccaaaccattgatccatcactgaagtoaaagagc
genomic_hu	1	-----
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genomic_hu	1	-----
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genomic_hu	1	-----
cDNA_rat	1551	ataaggccgacatgggtctgtagtatocaaaagccatcaaggacatcacca
genomic_hu	1	-----
cDNA_rat	1601	actgcattcactgaagaaaatgactacatcatgotaaatgogtcattttc
genomic_hu	1	-----
cDNA_rat	1651	cacaaatottgtgtgcagtgtagattataatcacatccagccagtggtggc
genomic_hu	1	-----
cDNA_rat	1701	aaottctggctttatacagtgactctcctotgatactagaagggaagccc
genomic_hu	1	-----
cDNA_rat	1751	cagcttaccgagactccttcactgtcttctagatataaacagggtggotot
genomic_hu	1	-----
cDNA_rat	1801	taggctgaagacattttaccagcatagaggctgatgtcagagcagacc
genomic_hu	1	-----
cDNA_rat	1851	ctttttggtccaacaagaaaaattgtcttgagctgaacagaactgccc
genomic_hu	1	-----
cDNA_rat	1901	accacacttagcacattacagatccagttttccactgatgtcctaaatcgc
genomic_hu	1	-----
cDNA_rat	1951	tttaccaggcgagatgagagcggagagactcaaatggacatgatcc
genomic_hu	1	-----

00005120-042202

cDNA_rat	2001	tgatgatgaacaatcccaaatggaacgcaactgtctgttgccggcact
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cDNA_rat	2051	attgccotgagctgtccaggcaaggcgaccccttcacctcacttggatg
genomic_hu	1	-----
cDNA_rat	2101	gottotagctgatgggagtaaagtgagagcccttaogttagcgaggatg
genomic_hu	1	-----
cDNA_rat	2151	ggcgaatccctaataagacaaaaatgggaagttggaactgcagatggctgac
genomic_hu	1	-----
cDNA_rat	2201	agctttgatgagggtotttaccactgcataagcaccaatgatgcagatgc
genomic_hu	1	-----
cDNA_rat	2251	ggatgtttcacatacaggataaactgtggtagagccctatggagaaagca
genomic_hu	1	-----
cDNA_rat	2301	cacatgacagtggagtcacagcacacagtgttaccgggtgagacgctcgao
genomic_hu	1	-----
cDNA_rat	2351	cttccatgcctttccacgggtgttccagatgcttotattagctggattct
genomic_hu	1	-----
cDNA_rat	2401	tccagggaacactgtgttctctcagccatcaagagacaggcaattctta
genomic_hu	1	-----
cDNA_rat	2451	acaatgggaccttaagaatattacaggttacgcacaaagatoaaggtoat
genomic_hu	1	-----
cDNA_rat	2501	taccaatgtgtggtgccaacccatcaggggccgacttttccagttttaa
genomic_hu	1	-----
cDNA_rat	2551	agtttcagttcaaaagaaaggccaaaggatggttgagcatgcaggagg
genomic_hu	1	-----
cDNA_rat	2601	caggtgatctggacttggagaacccaaactccagtgttcccttaagcag
genomic_hu	1	-----
cDNA_rat	2651	ccagcatctttgaaactctctgcacagctttgacagggtcagaggctgg
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genomic_hu	1	-----
cDNA_rat	2751	atcggcggcggtggggattccacgctccgagcattcaggagcataggagg
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genomic_hu	1	-----
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cDNA_rat	2951	gaaaaggatgcctctggcatgattcctccagatgaagaattcatggttct
genomic_hu	1	-----

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genomic_hu	1	-----
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genomic_hu	1	-----
cDNA_rat	3101	tcaactgtgaatocacaaacactaactctgagcaccttootgatttcaa
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genomic_hu	1	-----
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genomic_hu	1	-----
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cDNA_rat	3901	gttactatttaaggacaaacaaaatgtagatattgagataatacaacca
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cDNA_rat genomic_hu	4251 1	tacaaaagaaccagccgcaaagcttcccaaatagctcctotttttacco
cDNA_rat genomic_hu	4301 1	acaggtcagagttccccctcagattctacaactctcttgacaagtcggoc
cDNA_rat genomic_hu	4351 1	accagctctgtctacaacaatgggtgccactcagaacaagggcactgaag
cDNA_rat genomic_hu	4401 1	tagtatacaggtgccagaagtctctcagcagggagaagcagcccttcaoo
cDNA_rat genomic_hu	4451 1	aactcctotccagtgttccctagcaccataagcaagagatctaatacatt
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cDNA_rat genomic_hu	5251 1	tgagaagggcaaaaggccagcagtaagcatgtcccccaacctcagccttc -----
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cDNA_rat genomic_hu	6201 1	tgtatataagaagcatogctccttcagtgggggcaacttatgagtgcat -----
cDNA_rat genomic_hu	6251 1	gccaccagctcctcaggctcagagagaagggtagtgattcttactgtgga -----

00005430 04200

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cDNA_rat	6351	aggtgaatttgggtgagaaattactactgaactgctcagctactggggat
genomic_hu	1	-----
cDNA_rat	6401	ccaaagcctagaataatctggaggctgccatccaaggctgtcatogacca
genomic_hu	1	-----
cDNA_rat	6451	gtggcacagaaTGGGCAGCCGAATCCACGTCTACCCAAATGGATCCTTGg
genomic_hu	1	-----TGGGCAGCTGGATCCACGTCTACCTAATGGATCCCTGT
cDNA_rat	6501	tggttgggTCAGTGACGGAAAAAGACGCTGGTGACTACTTATGTGTGGCA
genomic_hu	40	ttattggaTCAGTAACAGAAAAAGACAGTGGTGTCTACTTGTGTGTGGCA
cDNA_rat	6551	AGAAACAAATGGGAGATGACCTAGTCCTGATGCATGTccgcctgAGATT
genomic_hu	90	AGAAACAAATGGGGATGATCTGATACTGATGCATGTtagcctaAGACT
cDNA_rat	6601	GACACCTGCCAAATTGAACAGAAGCAGTATTTTAagAAGCAAGTGCTCC
genomic_hu	140	GAAACCTGCCAAATTGACCACAAGCAGTATTTTAgaAAGCAAGTGCTCC
cDNA_rat	6651	ATGGGAAGATTTCCAAGTTGACTGCAaggcctotGGCTCCCCGTGTCCT
genomic_hu	190	ATGGGAAGATTTCCAAGTAGATTGCAaagcttccGGCTCCCCAGTGCCA
cDNA_rat	6701	GAGGTATCCTGGAGTTTGCCTGATGggacagtgcTCAACATGTAGCCCA
genomic_hu	240	GAGATATCTTGGAGTTTGCCTGATGgaacoatgaTCAACATGCAATGCA
cDNA_rat	6751	AGCTGATGACAGTGGCTATAGGACcaagaggtacACCCTTTTCACAATG
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cDNA_rat	6801	GAACCTTGTATTTCAACAACGTTGggatggcaGAGGAAGGAGATTATATC
genomic_hu	340	GAACCTTATACTTCAACAAGTTGgggtagcgGAGGAAGGAGATTATACT
cDNA_rat	6851	TGCTCTGCCAGAACACCTTAGGGAAAGATGAGATGAAAGTCCACCTAAC
genomic_hu	390	TGCTATGCCAGAACACCCCTAGGGAAAGATGAAATGAAGGTCCACTTAAC
cDNA_rat	6901	AGTTCTAACAGCcatcCCACGGATAAGGCAAAGCTACAAGACCACCATGA
genomic_hu	440	AGTTATAACAGCtgotCCCCGATAAGGCAGAGTAACAAAACCAACAAGA
cDNA_rat	6951	GGCTCaggGCTGGAGAAACAGCTGTCTTGAAGTGGAGGTCAGTGGGGaa
genomic_hu	490	GAATCAaaGCTGGAGACACAGCTGTCTTGAAGTGGAGGTCAGTGGGGat
cDNA_rat	7001	ccgaagccaatgTATTTTGGTTGCTGCCTTCCAAcaatgtcATTTCATT
genomic_hu	540	cccaasccaaaaaTATTTTGGTTGCTGCCTTCCAAtagaatgATTTCCTT
cDNA_rat	7051	CTCCAATGACAGGTTACATTTTCATGCCAATagaaCTTTGTCCATCCATA
genomic_hu	590	CTCCATTGATAGGTACACATTTTCATGCCAATgggtCTTTGACCATCAACA
cDNA_rat	7101	AAGTGAAACCACTTGACTCTGGGGactatgtgtgcttagctcagAATCCT
genomic_hu	640	AAGTGAAACTGCTCGATTCTGGAGagtacgtatgtgtagcccgAATCCC
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genomic_hu	690	AGTGGGGATGACACCAAAATGTACAAACTGGatgtGTCTCTAAACCTCC
cDNA_rat	7201	ATTAATCAATGGCCTGTATGCAACAaagACTGTTATTAAAGCCACAGCca
genomic_hu	740	ATTAATCAATGGTCTGTATACAAACagaACTGTTATTAAAGCCACAGCtg
cDNA_rat	7251	ttcggcacTCCAAAAAATACTTTGACTGCAGAGCAGATGGGATCCCATct
genomic_hu	790	tgagacatTCCAAAAACACTTTGACTGCAGAGCTGAAGGGACACCATct
cDNA_rat	7301	tcccaggtcacGTGGATTATGCCAGGCAATATTTTCCTCCAGCTCCATA
genomic_hu	840	cctgaagtcacGTGGATCATGCCAGACAATATTTTCCTCACAGCCCCATA

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cDNA_rat	7351	CttTGAAGCAGAGTCACGGTCCATCCAAATGGAACCTTGGAgatgagga
genomic_hu	890	CtaTGAAGCAGAATCACAGTCCATAAAAATGGAACCTTGGAsattagga
cDNA_rat	7401	acatccGGCTTTCTGACTCTGCGGACTTCACCTGTGTGGttcggagcgag
genomic_hu	940	atgtgaGGCTTTTCAGATTGAGCCGACTTTATCTGTGTGGcccgaaatgaa
cDNA_rat	7451	ggaGGAGAGAGTGTGTGGTAGTGACGTTAGAAGTCTTAGAAATGCTGAG
genomic_hu	990	ggtGGAGAGAGCGTGTGGTAGTACAGTTAGAAGTACTGGAARTGCTGAG
cDNA_rat	7501	AAGACCAACATTGAGAAACCCATTCAACGAAAagtcacgcgccaagctg
genomic_hu	1040	AAGACCGACATTTAGAAATCCATTTAATGAAAAaatagttgccagctgg
cDNA_rat	7551	gcaagcccgtagCACTGAACTGCTCTGTGGATGGGAACCCCCACCTGAA
genomic_hu	1090	gaaagtccacAGCATTGAATTGCTCTGTGTGGTAACCCACCACTGAA
cDNA_rat	7601	attacCTGGATCTTACCTGACGGCACACAGTTTGCTAACAGACCacacaa
genomic_hu	1140	ataatCTGGATTTTACCAAATGGCACAGATTTTCCAATGGACCacaaag
cDNA_rat	7651	ttccccGTATCTGATGGCAGGCAATGGCTCTCTCATCCTTTACAAAgcaa
genomic_hu	1190	ttatcagTATCTGATAGCAAGCAATGGTTCTTTTATCATTTCTAAaocaa
cDNA_rat	7701	ctcggacaagtcAGGGAAGTATCGCTGTGCAGCCAGGAATAAGGTTGGC
genomic_hu	1240	ctcggggaggatgCAGGAAAATATCGCTGTGCAGCTAGGAATAAAGTTGGC
cDNA_rat	7751	TAcacgagaaactcatcctgttagagATTGGGCAGAAGCCAGTCATTCT
genomic_hu	1290	TAtattgagaaattagtcattattagaaATTGGCCAGAAGCCAGTTATTCT
cDNA_rat	7801	GACATACGAACCCAGGGatggtgaagagcgTCAGTGGGGAACCGTTATCAC
genomic_hu	1340	TACCTATGCACCCAGGGAcagtaaaaggoaTCAGTGGAGAATCTCTATCAC
cDNA_rat	7851	TGCATTGTGTCTGATGGgATCCCCAAGCCAAATGTCAAGTGGACTACA
genomic_hu	1390	TGCATTGTGTCTGATGGaATCCCTAAGCCAAATATCAATGGACTATG
cDNA_rat	7901	CCGGGTGGccATGTAATCGACAGGCCTCAAGTGGATGGAAAATACATAcT
genomic_hu	1440	CCAAGTGGtAtGTAGTAGACAGGCCTCAAATTAATGGGAAATACATaT
cDNA_rat	7951	GCATGAAATGGCACGCTGGTCATCAAGCAACAACAGCtcacgaccaAG
genomic_hu	1490	GCATGACAATGGCACCTTAGTCATTAAAGAAGCAACAGCttatgacagAG
cDNA_rat	8001	GAAATTATATCTGTAGGGCTCAAAACAGTGTGGCCAggcagttattagc
genomic_hu	1540	GAAACTATATCTGTAAGGCTCAAAATAGTGTGGTCAacactgattact
cDNA_rat	8051	gtgtCAGTGATGGTTGTGGCCTACCTCCCCGAATCATAAactacctACC
genomic_hu	1590	gttcCAGTAATGATTGTAGCCTACCTCCCCGAATTACAAatogtccACC
cDNA_rat	8101	CAGGAACATGCTCAGGAGGACAGGGGAAGCCatgCAGCTCCAetGTGTGG
genomic_hu	1640	CAGGAGTATTGTCAACAGGACAGGGGCAGCctttCAGCTCCACTGTGTGG
cDNA_rat	8151	CCTTGGGAATCCCCAAGCCaaAAGTCACCTGGGAGACGCCAAGACACTCC
genomic_hu	1690	CCTTGGGAGTTCCCAAGCCagAAATCACATGGGAGATGCCTGACCACTCC
cDNA_rat	8201	CTGCTCTCAaagcaacagcaagaaaaacccCATAGAAGTGAGATGCTTCA
genomic_hu	1740	CTTCTCTCAAcggcaagtaagagaggacacATGGAAGTGAGCAGCTTCA
cDNA_rat	8251	CCCACAAGGTACGCTgCTCATTGAGAATCTCCAAACCTCGGATTCCGGag
genomic_hu	1790	CTTACAAGGTACCTaGTCATTGAGAATCCCCAAACCTCCGATTCTGGga
cDNA_rat	8301	tcTATAAGTGCAGAGCTCAGAACCTACTTGGgacTGATTACGCAACAACT
genomic_hu	1840	taTACAAATGCACAGCAAGAACCCTTGgtagTGATTATGCAGCAACG
cDNA_rat	8351	TACATCCAGGTACTCTGACAGGAagggygagactaaaattcaacagaagt
genomic_hu	1890	TATATTCAAGTAATCTGACATGAAataataaagtcaacaacatctgggca

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cDNA_rat 8401 ccacatccacagggTTTATTTTGGGAAGAAGTTTAATCAAAGGCAGCCA
 genomic_hu 1940 gaa-----TTTATTTTGGGAAGAAGTTTAATCAAAGGCAGCCA

 cDNA_rat 8451 TAGGCATGTAAATGAgtcTGAATACATTACAGTATTAAATTTACAATGG
 genomic_hu 1979 TAGGCATGTAAATGAatttGAATACATTACAGTATTAAATTTACAATGA

 cDNA_rat 8501 ACATGCgatga-----GACTTGTAATGAAAGCATTGTGAAGTGAaaccg
 genomic_hu 2029 ACATGCaaaataaaaagGACTTGTAATGAAAGCATTGTGAAGTGAatgata

 cDNA_rat 8546 agtctctg-----TGGATCTCAAAGCAAACCTTAACTTAAGGCACCTTTg
 genomic_hu 2079 ctgattttatttaaTGGATCTCAAACCAAACCTTAACTTAAGGCACCTTTt

 cDNA_rat 8591 ATTTTGCCAAACAAATAATAACAAACattagagaaaaaatgattCACTA
 genomic_hu 2129 ATTTTGCCAAACAAATAACAATAAACaaccattgaaacgggtt----CACTA

 cDNA_rat 8641 CGAAATAACAAACGGCTAATGCACCTGAATTctcagtaaaaagacotttc
 genomic_hu 2175 TAAATAACAAATGGCTAATGTACCTGAATTtttcagtaaaaaaatgaac

 cDNA_rat 8691 tctcgctaacagttgCCAGCTGCCTCGTGTCTGTTTCTACCAATGTGAC
 genomic_hu 2225 ttctaata-----CCAGTTGCCTAGTGTCCACCTCCTATCAATGTTAC

 cDNA_rat 8741 AAACatogcacacagggTGAATGGAGTCAACGGGAAAGATTAAGTTTGGG
 genomic_hu 2268 AAGCATggcactca----GAACAGAGACAATGGAAATATTAATCTGCA

 cDNA_rat 8791 GTCTgtgtaaattctca-----ATGTACAAATATTCTGtcncTG
 genomic_hu 2314 ATCtttatgatgtaaatttaccatcctgATGTATAAATATTTTG----TG

 exon1 (2342-2397)
 cDNA_rat 8791 GTCTgtgtaaattctca-----ATGTACAAATATTCTGtcncTG
 genomic_hu 2314 ATCtttatgatgtaaatttaccatcctgATGTATAAATATTTTG----TG

 cDNA_rat 8829 GTTTATAAACATTTTGTATAAAACCGAAAAAAAAAAAAAAAAAAAAA
 genomic_hu 2360 GTTTATAAATTTTTTGTATAAACCTACAGAAATAAGcactgaactgtc

(Genomic human OCP: SEQ ID NO:4)
 (cDNA rat: SEQ ID NO:5)

24/90

Figure 11

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length	Remarks
1	1	208	208	69	No valid splice site found upstream this exon
2	277	429	153	18	
3	447	485	39	1561	
4	2046	2244	199	1351	
5	3595	3724	130	3254	
6	6978	7359	382	4123	
7	11482	14903	3422	38	
8	14941	15307	367	51	
9	15358	15825	468	1039	
10	16864	~17760	~897	?	Last exon might be complete
11	?(1)	2317	~231 7	25	Exon is not complete and start site is not known
12	2342	2397	56	-	

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FIGURE 12

608 Human translated nucleotide sequence (ORF)

ATGAAGGTAAAAGGCAGAGGAATCACCTGCTTGGTCTCCTTTGCTGT
GATCTGCCTGGTCGCCACCCCTGGGGCAAGGCCTGCTCGCCGCTGTG
CCTGTTATATGCCTACGGAGGTACACTGCACATTTGCGGTACCTGACTTCCA
TCCCAGACAGCATCCCGCCCAATGTGGAACGCATCAATTTAGGATACAAC
AGCTTGGTTAGATTGATGGAACAGATTTTCTGGCCTGACCAAACTGGA
GTTACTCATGCTTCACAGCAATGGCATTACACAATCCCTGACAAGACCTT
CTCAGATTTGCAAGCCTTGCAGGTCTTAAAAATGAGCTATAATAAAGTCC
GAAAACTTCAGAAAGATACTTTTATGGCCTCAGGAGCTTGACACGATTG
CACATGGACCACAACAATATTGAGTTTATAAACCCAGAGGTTTTTATGG
GCTCAACTTTCTCCGCTGGTGCATTGGAAGGAAATCAGCTCACTAAGCT
CCACCCAGATACATTTGTCTCTTGGAGCTACCTCCAGATATTTAAAAATCTC
TTTCATTAAAGTTCCTATACTGTCTGATAACTTCTGACCTCCCTCCCTCAA
GAGATGGTCTCCTATATGCCTGACCTAGACAGCCTTACCTGCATGGAAG
CCCATGGACCTGTGATTGCCATTAAAGTGTTGTCTGACTGGATACAGCC
AGATGTAATAAAATGCAAAAAAGATAGAAGTCCCTCTAGTGCTCAGCAGT
GTCCACTTTGCATGAACCCCTAGGACTTCTAAAGGCAAGCCGTTAGCTATG
GTCTCAGCTGCAGCTTTCCAGTGTGCCAAGCCAACCATTTGACTCATCCCTG
AAATCAAAGAGCCTGACTATTCTGGAAGACAGTAGTTCTGCTTTCATCTCT
CCCCAAGGTTTCATGGCACCCCTTTGGCTCCCTCACTTTGAATATGACAGAT
CAGTCTGGAAATGAAGCTAACATGGTCTGCAGTATTCAAAGGCCCTCAAG
GACATCACCCATTGCATTCACTGAAGAAAATGACTACATCGTGCTAAATA
CTTCATTTTCAACATTTTGGTGTGCAACATAGATTACGGTCACATTACAGC
CAGTGTGGCAAAATTTGGCTTTGTACAGTGATTCTCCTCTGATACTAGAAA
GGAGCCACTTGCTTAGTGAAACACCGCAGCTCTATTACAAATATAAACAG
GTGGCTCCTAAGCCTGAAGACATTTTACCAACATAGAGGCAGATCTCAG
AGCAGATCCCTCTTGGTTAATGCAAGACCAAAATTTCTTGCAGCTGAACA
GAAGTGGCAACACATTCACTACATTACAGATCCAGTACTCCAGTGATGCT
CAAATCACTTTACCAAGAGCAGAGATGAGGCCAGTGAAACACAAATGGA
CTATGATTTCAAGGGATAACAATACTAAGCTGGAACATACTGTCTTGGTA
GGTGGAAACCGTTGGCCTGAACTGCCAGGCCAAGGAGACCCCAACCCACA
CGTGGATTGGCTTCTAGCTGATGGAAGTAAAGTGAGAGCCCTTATGTCA
GTGAGGATGGACGATCCTAATAGACAAAAGTGGAATTTGGAATCCA
GATGGCTGATAGTTTGTACACAGGCGTATATCACTGTATAAGCAGCAATT
ATGATGATGCAGATACTCTACCTATAGGATAACTGTGGTAGAACCTTTGG
TCGAAGCCTATCAGGAAAATGGGATTCATCACACAGTTTTCATTGGTGAA
ACACTTGATCTTCCATGCCATTCTACTGGTATCCAGATGCCTCTATTAGC
TGGGTTATTCCAGGAAACAATGTGCTCTATCAGTCATCAAGAGACAAGAA
AGTTCTAAACAATGGCACATTAAGAATATTACAGGTACCCCCGAAAGACC
AAGGTTATTATCGCTGTGTGGCAGCCAACCCATCAGGGGTTGATTTTGA
TTTTCCAAGTTTCAGTCAAGATGAAAGGACAAAGGCCCTTGGAGCATGAT
GGAGAAACAGAGGGATCTGGACTTGATGAGTCCAATCCTATTGCTCATCT
TAAGGAGCCACCAAGGTGCACAACCTCCGTAACATCTGCTCTGATGGAGGCTG
AGGTTGGAAAAACACACCTCAAGCACAAAGTAAGAGGCACAACATCGGGA
ATTAACTCCACGCGACGTGGAGATTCAACACATCGACGTTTATGGGAGA
ATAGGAGGCATTTCCTCCCTCTGCTAGGAGAATTGACCCACAACATTGG
GCGGCACTGTTGGAGAAAGCTAAAAAGAATGCTATGCCAGACAAGCGAG
AAAATACCACAGTGAGCCCAACCCCAAGTGGTCAACCAACTCCCAACATA
CCTGGTGAAGAAGACGATTCTCAGGCATGCTCGCTCTACATGAGGAATT

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TATGGTCCCGGCCACTAAAGCTTTGAACCTTCCAGCAAGGACAGTGACTG
CTGACTCCAGAACAATATCTGATAGTCCTATGACAAACATAAATTATGGC
ACAGAATTCTCCTGTTGTGAATTCACAAATACTACCACCTGAAGAACC
ACAGATTTCAAAGTGTCTACTGCTATTAATACTACAGCCATGTCAAAGAA
TATAAACCCCAACCATGTCAAGCCAAATACAAGGCACAACCAATCAACATT
CATCCACTGTCTTTCCACTGCTACTTGGAGCAACTGAATTTCAAGACTCTG
ACCAGATGGGAAGAGGAAGAGAGCATTTCCAAAGTAGACCCCCAATAAC
AGTAAGGACTATGATCAAAGATGTCAATGTCAAAATGCTTAGTAGCACC
CCAACAACTATTATTAGAGTCAGTAAATACCACAAATAGTCATCAGACA
TCTGTAAGAGAAGTGAGTGAACCCAGGCACAATCACTTCTATTCTCACAC
TACTCAAATACTTAGCACCTCCACGTTCCCTTCAGATCCACACACAGCTGC
TCATTCTCAGTTTCCGATCCCTAGAAATAGTACAGTTAACATCCCGCTGTT
CAGACGCTTTGGGAGGCAGAGGAAAAATTGGCGGAAGGGGGCGGATTATC
AGCCCATATAGAACTCCAGTTCTGCGACGGCATAGATACAGCATTTCAG
GTCAACAACCAGAGGTTCTTCTGAAAAAAGCACTACTGCATTCTCAGCCA
CAGTGCTCAATGTGACATGTCTGTCTCTTCCCAGGGAGAGGCTCACCA
CTGCCACAGCAGCATTGTCTTTCCAAAGTGCTGCTCCCATCACCTTCCCCA
AAGCTGACATTGCTAGAGTCCCATCAGAAGAGTCTACAACCTTAGTCCAG
AATCCACTATTACTACTTGAGAACAACCCAGTGTAGAGAAAAACAACACC
CACAATAAAATATTTCAAGGACTGAAATTTCCCAAGTGACTCCAAGTGGTG
CAGTCATGACATATGCTCCAACATCCATACCCATGGAAAAAACTCACAAA
GTAAACGCCAGTTACCCACGTGTGTCTAGCACCAATGAAGCTAAAAGAGA
TTCAGTGATTACATCGTCACTTTCAAGGTGCTATCACCAGCCACCAATGAC
TATTATAGCCATTACAAGGTTTTCAAGAAGGAAAAATCCCTGGCAACAGA
ACTTTGTAAATAACCAATAACCCAAAAGGCAGATTAAAGGAATCAACATAAA
GTTAGTTTACAAAAAAGCACAGCTGTGATGCTTCTTAAAAACATCTCCTGCT
TTACCACAGAGACAAAGTTCCCTTTCCATTTACCACACTTTCAACAAGT
GTGATGCAAATTCATCTAATACCTTGACTACCGCTCACCACACTACGACC
AAAAACACAATCCTGGAAGTCTTCAACAAGAAGGAGCTTCCCTTCCC
ACCCCTTAACCTATGCTTCCCTAGTATTATAAGCAAAGACTCAAGTACAA
AAAGCATCATATCAACGCAACAGCAATACCAGCAACAACCTCTACCTTC
CCTGCATCTGTCTCACTTATGAAACCCAAACAGAGAGATCTAGAGCACA
AACAAATACAAAAGAGAACAGGAGCCTCAAAAAGAAACAGGACTGACCCA
AACATCTCTCCAGACCAGAGTTCTGGCTTCACTACACCCACTGCTATGACA
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TCAAGCACAATCAGTTTTCACTCAAGAACTCTTAATCTGACAGATGTGATT
GAAGAACTAGCCCAAGCAAGTACTCAGACTTTGAAGAGCACAATTGCTTC
TGAAACAACCTTTGTCCAGCAAAATCACACCAGAGTACCACAACCTAGGAAAG
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GTGGCGACTCCCATTTCCGGCTTATGACAAATACAGTGGTCAAGCTGCAC
GAATCCTCAAGGCACAATCTCCAAATGCCAAGTTCACAATTGGAACCACT
CACTTCATCTACCTCTAATCTGTTACATTCTACTCCCATGCCAGCACTAAC
AACAGTTAAATCACAGAATTCCAAATTAACCTCATCTCCCTGGGCAGAAT
ACCAATTTTGGCACAAACCACTACTCAGACATTGCTGAAAAAGGCAAAAAG
CCAGAAGTAAGCATGTTGGCTACTACAGGCCTGTCCGAGGCCACCACTCT
TGTTTCAGATTGGGATGGACAGAAGAACAACAAGAAGAGTGACTTTGATA
AGAAACCAGTTCAAGAAGCAACAACCTCCAAACTCCTTCCCTTTGACTCTT
TGTCTAGGTATATATTTGAAAAGGCCAGGATAGTTGGAGGAAAAAGCTGCA
AGTTTTACTATTCCAGCTAACTCAGATGCCTTTCTTCCCTGTGAAGCTGTT

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GGAAATCCCCTGCCCACCATTTCATTGGACCAGAGTTTCAGGACTTGATTTA
TCTAGAGGAAAACCAGAATAGCAGGGTCCAGGTTCTCCCAATGGTACCCT
GTCCATCCAGAGGGTGGAAATTCAGGACCGCGACAGTACTTGTGTCCG
CATCCAATCTGTTTGGCACAGACCACCTTCATGTCACCTTGTCTGTGGTTT
CCTATCCTCCCAGGATCCTGGAGAGACGTACCAAAGAGATCACAGTTCAT
TCCGGAAGCACTGTGGAAGTGAAGTGCAGAGCAGAAGGTAGGCCAAGCC
CTACAGTTACCTGGATTCTTGCAAACCAAACAGTTGTCTCAGAATCATCCC
AGGGAAGTAGGCAGGCTGTGGTGACGGTTGACGGAACATTGGTCCTCCAC
AATCTCAGTATTTATGACCGTGGCTTTTACAAATGTGTGGCCAGCAACCA
GGTGGCCAGGATTCAGTGTGGTTAAAAATACAAGTCATTGCAGCACCACC
TGTTATTCTAGAGCAAAGGAGGCAAGTCATTGTAGGCACTTGGGGTGAAA
GTTTAAACTGCCCTGTACTGCAAAGGAACTCCTCAGCCCAGCGTTTACT
GGGTCCTCTCTGATGGCACTGAAAGTGAACCAATTACAGTTTACCAATTCCA
AGTTGTTCTTATTTCAAATGGGACTTTGTATATAAGAAACCTAGCCTCTT
CAGACAGGGGCATTATGAATGCATTGCTACCAGTTCCACTGGTTCGGAG
CGAAGAGTAGTAATGCTTACAATGGAAGAGCGAGTGACCAGCCCCAGGA
TAGAAGCTGCATCCCAGAAAAGGACTGAAGTGAATTTGGGGACAAATTA
CTACTGAACTGCTCAGCCACTGGGGAGCCCCAAACCCCAAATAATGTGGAG
GTTACCATCCAAGGCTGTGGTCGACCAGTGGAGCTGGATCCACGTCTACC
CTAATGGATCCCCTGTTTATTGGATCAGTAACAGAAAAGACAGTGGTGTC
TACTTGTGTGTGGCAAGAAACAAAATGGGGGATGATCTGATACTGATGCA
TGTTAGCCTAAGACTGAAACCTGCCAAAATTGACCACAAGCAGTATTTTA
GAAAGCAAGTGCTCCATGGGAAAGATTTCCAAGTAGATTGCAAAGCTTCC
GGCTCCCCAGTGCCAGAGATATCTTGGAGTTTGCTGATGGAACCATGAT
CAACAATGCAATGCAAGCCGATGACAGTGGCCACAGGACTAGGAGATAT
ACCCTTTTCAACAATGGAACCTTATACTTCAACAAAGTTGGGGTAGCGGA
GGAAGGAGATTATACTTGTATGCCCAGAACACCCTAGGGAAAGATGAA
ATGAAGGTCCACTTAACAGTTATAACAGCTGCTCCCGGATAAGGCAGAG
TAACAAAACCAACAAGAGAATCAAAGCTGGAGACACAGCTGTCCTTGACT
GTGAGGTCACTGGGGATCCCAAACCAAAAATATTTTGGTTGCTGCCTTCC
AATGACATGATTTCTCTCCATTGATAGGTACACATTTTCATGCCAATGGG
TCTTTGACCATCAACAAAGTGAAGTCTCGATTCTGGAGAGTACGTATG
TGTAGCCCGAAATCCCAGTGGGGATGACACCAAAATGTACAAACTGGATG
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TTAAAGCCACAGCTGTGAGACATTCCAAAAACACTTTGACTGCAGAGCT
GAAGGGACACCATCTCTGAAGTCATGTGGATCATGCCAGACAATATTTT
CCTCACAGCCCCATACTATGGAAGCAGAATCACAGTCCATAAAAAATGGAA
CCTTGAAAATTAGGAATGTGAGGCTTTCAGATTACAGCCGACTTTATCTGTG
TGGCCCGAAATGAAGGTGGAGAGAGCGTGTGGTAGTACAGTTAGAAGTA
CTGGAATGCTGAGAAGACCGACATTTAGAAAATCCATTTAATGAAAAAT
AGTTGCCAGCTGGGAAAGTCCACAGCATTGAATTGCTCTGTTGATGGTA
ACCCACCACCTGAAATAATCTGGATTTTACCAAATGGCACACGATTTTCCA
ATGGACCACAAAGTTATCAGTATCTGATAGCAAGCAATGGTTCTTTTATCA
TTTCTAAAACAACTCGGGAGGATGCAGGAAAATATCGCTGTGCAGCTAGG
AATAAAGTTGGCTATATTGAGAAATTAGTCATATTAGAAATTGGCCAGAA
GCCAGTTATTCTTACCTATGCACCAGGGACAGTAAAAGGCATCAGTGGAG
AATCTCTATCACTGCAATTGTGTGTCTGATGGAATCCCTAAGCCAAATATCA
AATGGACTATGCCAAGTGGTTATGTAGTAGACAGGCCTCAAATTAATGGG
AAATACATATTGCATGACAATGGCACCTTAGTCATTAAAGAAAGCAACAGC
TTATGACAGAGGAAACTATATCTGTAAGGCTCAAAATAGTGTGGTCATA

[illegible]

29/90
Figure 13

A

Region			Region Length	% identity	% positives	% gaps
General	Rat	Human				
1-655	1-655	1-653	655	76	86	0
656-726	656-726	654-724	71	46	62	0
727-779	727-779	725-777	53	77	86	0
780-1634	780-1617	778-1612	655	38	53	4
1635-end	1618-end	1613-end	980	74	85	0
	Total	Alignment	2614	62	74	1

B

Region			% identity	% positives	% gaps
Rat	Mouse	Length			
1-238	1-238	238	91	92	1

C

Region			Region Length	% identity
General	Rat	Human		
1-1965	1-1965	1-1965	1965	83
1966-2178	1966-2178	1966-2178	213	86
2179-2337	2179-2337	2179-2337	159	86
2338-4893	2338-4893	2338-4863	2565	63
4894-7833	4852-7791	4864-7761	2940	80
	Total	Alignment	7842	80

D

Region			Region Length	% identity
General	Rat	Mouse		
1-720	1-718	1-720	720	93

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[illegible][illegible]

rat_cDNA
human 5+3 corrected
mus_cDNA_5

AGCCTTACTAGATTGACAGAAAAAGACTTTGATGGCTGAGCAAACTGGAGTTACTCATG
AGCTTGGTTAGATTGATGGAAACAGATTTTCTGGCTGACCAAACTGGAGTTACTCATG
AGCCTCACTAGATTGACAGAAAAAGACTTTTCTGGCTGAGCAGACTGGAGTTACTCATG
*** * ***** **

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CTGCACAGTAATGGCATTACAGAGTCAGTGACAAGACCTTCTCGGGCTTGCACTGCTG
CTTCACAGCAATGGCATTACACCAATCCTGACAGACCTTCTCAGATTGTCAGGCTTG
CTGCACAGCAATGGCATTACAGAGTCAGTGACAAGACCTTCTCGGGCTTGCACTGCTG
** ***** **

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CAGGTCTTAAAAATGAGCTATAACAAAGTCCAAATCATTGGGAGGATACTTTCTACGGA
CAGGTCTTAAAAATGAGCTATAATAAAGTCCGAAACCTTCAGAAAGATCTTTTATGGC
CAGGTCTTAAAAATGAGCTATAACAAAGTCCAAATCATTGAGAGGATACTTTGATGGA
***** **

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CTCGGAGCTTGGTCCGGTTGCACCTGGATCACAACAACATTGAATTCATCAACCTGAG
CTCAGGAGCTTGACAGATTGCACATGGACCAACAATATTGAGTTTATTAACCCAGAG
CTCAGGAGCTTGACCCGGTTGCACCTGGATCACAACAACATTGAGTTTATCAACCCAGAG
*** ***** **

rat_cDNA
human 5+3 corrected
mus_cDNA_5

GCTTTTATGGACTTACCTCGCTCCGCTTGGTACATTAGAGGAAACCGGCTCACAAG
GTTTTTATGGGCTCACTTTCTCCGCTGGTGCCTTGGAGGAAATCAGCTCACTAAG
GGTTTTACGGACTCACCTTGCCTCCGCTTGGTACATCTAGAGGAAACCGGCTCACAAG
* ***** **

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CTCCATCCAGACACATTGTCTCTTAAGCTATCTCCAGATATTTAAACCTCTTTTCATT
CTCCACCCAGATACATTGTCTCTTGGAGTACCTCCAGATATTTAAACCTCTTTTCATT
CTCCATCCAGACACATTGTCTCTTGGAGTATCTCCAGATATTTAAACCTCTTTTCATT
***** **

rat_cDNA
human 5+3 corrected
mus_cDNA_5

AAGTACCTGTCTTGTCTGATAACTTCT-GACCTCCCTCCCAAAGAAATGGTCTCCTA
AAGTCTCTATCTGTCTGATAACTTCT-GACCTCCCTCCCTCAAGAGATGGTCTCCTA
AAGNACCTGTACTGTATGATAACTTCTTGAACCTCCCTCCCAAAGAAATGGTCTCCTC
*** **

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CATGOCAAACCTAGAAAGCCTGTATTGTCATGGAAACCCATGGACCTGTGACTGCCATT
TATGCTGACCTAGACAGCCTTTACCTGCATGGAAACCCATGGACCTGTGACTGCCATT
TATGOCAAACCTAGAAAGCCTTTACTTGCATGGAAACCCATGGACCTGTGACTGCCATT
***** **

rat_cDNA
human 5+3 corrected
mus_cDNA_5

AAAGTGGTTGTCTGAGTGGATGCAGGGAACCCAGATATAATAAATGCAAGAAAGACAG
AAAGTGGTTGTCTGACTGGATACAGGNNNNOCAGATATAATAAATGCAAAAGATAG
AAAGTGGTTGTCCGAGTGGATGCAGGGAACCCAGGTA-ACTATCTTGT---TTGTTG
***** **

rat_cDNA
human 5+3 corrected
mus_cDNA_5

AAGCTCTTCCAGTCTCAGCATGTCCCT-TTGCATGAACCCAGGATCTCTAAGGCA
AAGTCCCTCTAGTCTCAGCAGTGTCCACT-TTGCATGAACCCAGGACTCTAAGGCA
TTTCTTTTTTATARKAGTATTTTCTCAATTCATTAGAAATGATATCCAAAGTC-
* * * * *

rat_cDNA
human 5+3 corrected
mus_cDNA_5

GACCTTTGCTATGGTACCATCTGGAGCTTTCTATGTACAAAGCCACCATTTGATCCAT
AGCCGTTAGCTATGGTCTCAGCTGCAGCTTCCAGTGTGCCAAGCCACCATTTGATCCAT
-CCCATAACTCCCTCCCA-CTTCCCTACCTACCATTC-CCATTTTGTGGC
* * * * *

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CAGTGAAGTCAAAGAGCCTGGTTACTCAGGAGGACATGGATCTGCTCCACTCACTC
CCTGAAATCAAAGAGCCTGACTATTCTGGAGACAGTAGTCTGCTTTCTCTCTCCCC
CTGGCATTCCTC-----
* * * * *

rat_cDNA
human 5+3 corrected
mus_cDNA_5

AAGATTTATAGAACCTTTGGCTCCTGTCTTTGAACATGACANNTNTCTGGAATA
AAGTTTATGGCACTTTGGCTCCTCATTGAAATATGACAGATCAGTCTGGAATG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

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AAGCTAATCATGGTCTGCAGTATTCAAAGCCTCAAGGACATCAACCACTGCATTCACTG

00005429:042202

rat_cDNA
human 5+3 corrected
mus_cDNA_5

AAGAAAATGACTACATCATGCTAAATGGGTCTTTTCCACAAATCTTGTGTGAGTGTAG
AAGAAAATGACTACATCGTGTAAATACTTCATTTTCAACATTTTGGTGTGCAACATAG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

ATTATAATCACATCCAGCCAGTGTGGCACTTCTGGCTTTATACAGTGAAGTCTCTCTGA
ATTACGGTCACATTCAGCCAGTGTGGCAATTTTGGCTTTGTACAGTGAATCTCTCTGA

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TACTAGAAAGGAAGCCCGAGCTTACCGAGACTCCTTCACTGTCTTCTAGATATAAACAGG
TACTAGAAAGGAGCCACTTGCTTAGTGAACACCGCAGCTCTATTACAATATAAACAGG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TGGCTCTTAGGCGTGAAGACATTTTACCAGCATAGAGGCTGATGTGAGAGCAGACCCCTT
TGGCTCTTAGGCGTGAAGACATTTTACCAGCATAGAGGCTGATGTGAGAGCAGATCCCT

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TTTGGTTCCACAAAGAAAATTTGTCTTGAGCTGAACAGAACTGCCACCACTTAGCA
CTTGGTTAATGCAAGACCAATTTCTTGAGCTGAACAGAACTGCCACCACTTAGCA

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CATTACAGATCCAGTTTCCACTGATGCTCAAATCGCTTTACCAAGGGCGGAGATGAGAG
CATTACAGATCCAGTACTCCAGTGAATGCTCAAATCACTTTACCAAGGCGAGAGATGAGG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CGGAGAGACTCAAATGGACCATGATCTGATGAACAAATCCAACTGGAAAGCACTG
CAGTGAACACAAATGGACTATGATTTCAAGGGATAACATACTAAGCTGGAACTACTG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TCTTGGTTGGCGGCACTATTGCGCTGAGCTGTCCAGGCAAGGGGCACTTCACTCACT
TCTTGGTAGGTGGAACTGCTGGAAGTCCAGGCAAGGGGCACTTCACTCACT

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TGGAATGGCTTCTAGCTGATGGGAGTAAAGTGAGAGCCCTTACGTTAGGAGGATGGG
TGGAATGGCTTCTAGCTGATGGGAGTAAAGTGAGAGCCCTTATGTCAGTGGGATGGG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

GAATCTAATAGACAAAATGGGAAGTTGGAAGTGCAGATGGCTGACAGCTTTGATGAG
GGATCTAATAGACAAAATGGGAAGTTGGAAGTGCAGATGGCTGATAGTTTGGACAG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

GTCTTTACCACTGCATAAGCAACATGATGCAGATGGGATGTTCTCACATACAGGATAA
GGTATATCACTGTATAAGCAGCAATTTATGATGATGCAGATTTCTCACCTATAGGATAA

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CTGTGGTAGAGCCCTATGGAGAAAGCACATGACAGTGGAGTCCAGCACAGTGGTTA
CTGTGGTAGAGCCCTTGGTGGAGCCCTATCAGGAAATGGGATTCATCACAGTGGTTA

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CGGGTGAGAGCGCTGACCTTCCATGCTTTCCAGGGTGTTCAGATGCTTCTATTAGCT
TTGGTGAAACACTTGATCTTCCATGCTTTCTACTGGTATCCAGATGCTTCTATTAGCT

rat_cDNA
human 5+3 corrected
mus_cDNA_5

GGATTCTTCCAGGGAACACTGTGTTCTCTCAGCCATCAAGAGACAGGCAATTCITAA
GGATTCTTCCAGGGAACACTGTGTTCTCTCAGCCATCAAGAGACAGGCAATTCITAA

00005430-042000

rat_cDNA
human_5+3 corrected
mus_cDNA_5

ATGGGACCTTAAGAATATTACAGGTTACGCCAAAAGATCAAGGTCATTACCAATGTGTGG
ATGGCACATTAAGAATATTACAGGTCACCCCGAAAGACCAAGGTTATTATCGCTGTGTGG

rat_cDNA
human_5+3 corrected
mus_cDNA_5

CTGCCAACCCATCAGGGGCGGACTTTTCCAGTTTAAAGTTTCAGTTCAAAGAAAGGCC
CAGCCAACCCATCAGGGGTTGATTTTTCAGTTTCCAGTTTCAGTCAAGATGAAAGGAC

rat_cDNA
human_5+3 corrected
mus_cDNA_5

AAAGGATGGTTGAGCATGACAGGGAGGCGAGGTGGATCTGGACTTGGAGAACCCAACTCCA
AAAGGOCCTTGGAGCATGATGGAGAACAGAGGGATCTGGACTTGGATGAGTCCAACTCCA

rat_cDNA
human_5+3 corrected
mus_cDNA_5

GTGTTTCCCTTAAGCAGCCAGCATCTTTGAACTCTCTGCATCAGCTTTGACAGGGTCAG
TTGCTCATCTTAAGGAGCCACAGGTGACCACTCCGTACATCTGCTGATGGAGGCTG

rat_cDNA
human_5+3 corrected
mus_cDNA_5

AGGCTGGAACAAAGTCTCCGGTGTACATAGGAAGAACAAACATAGAGACTTAATACATC
AGGTTGGAACAAACACCTCAAGCACAAAGTAAGAGGCACAACTATCGGAATTAACACTCC

rat_cDNA
human_5+3 corrected
mus_cDNA_5

GGCGGCGTGGGGATCCACGCTCCGGGCAITCAGGAGCATAGGAGGCAGCTCCCTCTCT
AGCGAOGTGGAGATTCAACACATCGACGTTTATGGGAGAAATAGGAGGCATTTCCTCCCT

rat_cDNA
human_5+3 corrected
mus_cDNA_5

CTGCTCGGAGAAATGACCCGCAACGCTGGGCGACCTTCTAGAAAAGCCAAAAGAAAT
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rat_cDNA
human_5+3 corrected
mus_cDNA_5

CTGTGCCAAAAGCAAGAAATACCAAGTAAGGCCAGTGCCTGCTGCTTCCCTCTG
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rat_cDNA
human_5+3 corrected
mus_cDNA_5

TGGAACCTCACTGACGAGGAAAGGATGCTCTGGCATGATTCCTCCAGATGAAGAATTCA
CAAACATACCTGTTGAAGAAGACGATTCTCAGGCATGCTCGCTCTACATGAGGAATTCA

rat_cDNA
human_5+3 corrected
mus_cDNA_5

TGGTTCTGAAACTAAGGCTTCTGCTGTCCAGGAAGGTCAOCCACTGCTGACTCTGGAC
TGGTCCCGGCCACTAAGCTTTGAACCTTCAGCAAGGACAGTGAATGCTGACTCCAGAA

rat_cDNA
human_5+3 corrected
mus_cDNA_5

CAGTAAATCATGTTTTATGAGAGTAAGCTTCTGGCACAGAGTCTCAACTGTGAATC
CAATATCTGATGCTCTATGACAAACATAAATTATGGCACAGAACTCTCGTTGTGAAT

rat_cDNA
human_5+3 corrected
mus_cDNA_5

CACAAACACTACATCTGAGCACCTTCTGATTTCAAAATTATTAGTGAACAAAGGTA
CACAAATACCTACCACTGAGGAACCCACAGATTTCAAAGTGTCTACTGCTATTAAGTA

rat_cDNA
human_5+3 corrected
mus_cDNA_5

CAGCTGTGACAAAGAGTATGAACCATCCATAGCAAGCAAAATAGAAGATACAAACACC
CAGCATGTCAAAGAAATATAAACCCAAOCCATGTCAAGCCAAATACAAGGCACAAOCCATC

rat_cDNA
human_5+3 corrected
mus_cDNA_5

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AATATTATCCACTGTCTTCCACTGCTACTTGGAGCAACTGAATTCAGGACTCTGACA

00005130-0122002

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rat_cDNA
human_5+3 corrected
mus_cDNA_5

TTCCAGGCCCCCTCAGCACCCCTCAATAACAA-----CAAGCACAAAATTCCTCAAAGA
TTTCAGGTGCTATCAOCCAGCCCAATGACTATTATAGCAATTACAGGTTTTCAGAA

rat_cDNA
human_5+3 corrected
mus_cDNA_5

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GGAAATTCCTGGCAACAGAACTTTGTAATAACCAATACCCAAAAGGCAGATTAAAGA

rat_cDNA
human_5+3 corrected
mus_cDNA_5

ATCCATATCAATTGGTTTACAAAAGAACCCAGCCGCAAGGTTCCCAAAATAGCTCCTC
ATCAACATAAAGTTAGTTTACAAAAAGCACAGCTGTGATGCTTCTTAAACATCTCCTG

rat_cDNA
human_5+3 corrected
mus_cDNA_5

TTTACCCACAG-GTCAGAGTTCOCCCTCAGATTCTACAACCTCTCTTGACAAGTCCGCA
CTTACCC-ACAGAGACAAAGTTCOCCCTTTCATTTACCCACACTTTCAACAAGTGTGATG

rat_cDNA
human_5+3 corrected
mus_cDNA_5

CCAGCTCTGTCTACAACAATGGCTGCCACTCAGAACAGGGCACTGAAGTAGTATCAGGT
CAAAATTCATCTAATACCTTGACTACCGCTCACCACTACGACCAAA--ACACACAA-T

rat_cDNA
human_5+3 corrected
mus_cDNA_5

GCCAGAAGTCTCTCAGCAGGGAAGAGCAGCCCTTCAOCCACTCCTCTCCAG-TGCTTCC
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rat_cDNA
human_5+3 corrected
mus_cDNA_5

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rat_cDNA
human_5+3 corrected
mus_cDNA_5

GACAAGTCTACTGCTACTGCTCTGTCTATGTCTGAAACCAACGAACAGATCCAA
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rat_cDNA
human_5+3 corrected
mus_cDNA_5

AGAAAGCAAAAGACCAATAAAGGGGCTCG---GAAGAACAGAAACCAACGCAACACAC
AGCACAACAAATACAAAGAGAAGGAOCTCAAAGAGAACAGGACTGACCCAAACATCTC

rat_cDNA
human_5+3 corrected
mus_cDNA_5

CCCCAGGCAGGTTTCTGGCTATAGTGCATCTACTCAGCTCTAACACAGCTGATACCCCTT
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rat_cDNA
human_5+3 corrected
mus_cDNA_5

GGCTTTCAGTCAATCCCAACGACAGATGATGGTGGAAATGTAGTGCAGTTGCTTATCA
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rat_cDNA
human_5+3 corrected
mus_cDNA_5

CTCAACAACCTCTCTCTGGCA---TAACTGAAGTGTGAG--AGTAC--AACCAGAC
TTCAAGAACTCTTAATCTGACAGATGTGATTGAAGAACTAGCCCAAGCAAGTACTCAGAC

rat_cDNA
human_5+3 corrected
mus_cDNA_5

TTTGGGAATACACAGCTTTGGAAACAACTGTTGTGAGCAATCACAGGAGGTACCAC
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rat_cDNA
human_5+3 corrected
mus_cDNA_5

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0005430-01200

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~~—CCTTCCAGAGGCCAGCACTCATGCTCACACTGGAATACACAGAAGCATGCAGAAAAGA
GOCTGTCCGAGGCCACCACTCTTGTTTCAGATTGGGATGGACAGAGAAACACAAAGAAGA~~

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CTCTACCTAAGACTGTATTGAAAAAGCCAGAATAATTGGAGGAAAGGCTGCAAGCTTTA
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TCATCCACTGGACCAGAGTTTCATCAGGANTTGAAATATCCCAAGGGACACAGAAAGGC
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CTGTGGT TTTTACCGGC AAGGATTTTGGACAGACATGTCAAGGAGATCACAGTTTCAT
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CAGCTOCCOCTGT CATTATAGAGCRAAGAGGCAAGCCATCGTTGGGGTTT TAGGTGGAA
CAGCAOCCACTGTTATTCTAGAGCRAAGAGGCAAGTCATTGTAGGCACTTGGGGTGAAA

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CTGATGGCACTGAAGTGAAACCAATTACAGTTTACCAATTCCAAGTTGTTCTTAATTTCAA

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CCAOCAGCTOCTCAGGCTCAGAGAGAAGGGTAGTGATTCTTACTGTGGAGAGGGAGAGA
CTAOCAGTTCCACTGGTTCGGAGCGAAGAGTAGTAATGCTTACAATGGAAGAGOGAGTGA

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CCAGCCCCAGGATAGAACTGCATCCCAGAAAAGGACTGAAGTGAATTTGGGGACAAAT

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TACTACTGAACTGCTCAGCCACTGGGGAGCCCAAAACCCCAATAATGTGGAGGTTAACCAT

CCAAGGCTGTGATGACCAAGTGGCAGAAATGGGCAGCGAATCCACGTCTACCCAAATG
CCAAGGCTGTGGTCGACCAAGTGG-----GCAGCTGGATCCACGTCTACCCCTAATG

GATCCTTGGTGGTTGGGTCAGTGACGGAAAAAGACGCTGGTGACTACTTATGTGTGGCAA
GATCCCTGTTTATTGGATCAGTAACAGAAAAAGACAGTGGTGTCTACTTGTGTGGCAA

GAAACAAATGGGAGATGACCTAGTCTGATGCATGTCGGCTGAGATTGACACCTGCA
GAAACAAATGGGGGATGATCTGATACGATGCATGTTAGCCTAAGACTGAAACCTGCCA

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 AAATTGAACAGAAAGCAGTATTTTAAAGCAAGTGCTCCATGGGAAAGATTTCOAAGTGG
 AAATTGAACACAGCAGTATTTTAAAGCAAGTGCTCCATGGGAAAGATTTCOAAGTGG

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 ACTGCAAGGCTCTGGCTCCCTGTGCTGAGGTATCTGGAGTTTGGCTGATGGGACAG
 ATTGCAAAGCTTCCGGCTCCCACTGCCAGAGATATCTTGGAGTTTGGCTGATGGAAOCA

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 TGCTCAACAATGTAGCCCAAGCTGATGACAGTGGCTATAGGACCAAGAGGTACACCCCTT
 TGATCAACAATGCAATGCAAGCCGATGACAGTGGCCACAGGACTAGGAGATATACCCCTT

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 TCCACAATGGAACTTGTATTTCACCAAGCTTGGGATGGCAGAGGAGGAGATTATATCT
 TCAACAATGGAACTTTATACCTTCAACAAGTTGGGGTAGGGAGGAGGAGATTATACCTT

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 GCTCTGCCAGAACACCTTAGGGAAAGATGAGATGAAGTCCACCTAACAGTTCTAACAG
 GCTATGCCAGAACACCTTAGGGAAAGATGAATGAAGTCCACTTAACAGTTATAACAG

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 CCATCCACGGATAAGGCAAGCTACAGACCCATGAGGCTCAGGGCTGGAGAACAG
 CTGCTCCCGGATTAAGGCAGAGTAACAAACCAACAGAGAAATCAAAGCTGGAGACAG

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 CTGTCTTGACTGCGAGGTCACTGGGAAACGAAGCCCAATGTATTTTGGTTGCTGCCTT
 CTGTCTTGACTGTGAGGTCACTGGGATCCCAAACCAAAATATTTTGGTTGCTGCCTT

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 CCAACAATGTCAATTCATTCTCCAATGACAGGTTCACATTTCAAGCAATAGAACTTTGT
 CCAATGACATGATTTCTCTCCATGTATAGGTACACATTTCAAGCAATGGGTCTTTGA

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 CCATCCATAAAGTGAAACCACTTGACTCTGGGACTATGTGTGCGTAGCTCAGAACTCTA
 CCATCAACAAGTGAAACTGCTCGATTCTGGAGAGTAAGTATGTGTAGCCCGAAATCCCA

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 GTGGGGATGACACTAAGACATACAACTGGACATTTCTCTAAACCTCCATTAAATCAATG
 GTGGGGATGACACCAAAATGTACAACTGGATGTGGTCTCTAAACCTCCATTAAATCAATG

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 GCCTGTATGCRAACAAGACTGTTATTAAAGCCACAGCCATTGCGCACTCCAAAAAATACT
 GTCTGTATACAAACAGAACTGTTATTAAAGCCACAGCTGTGAGACATTCAAAAAATCACT

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 TTGACTGCAGAGCAGATGGGATCCCATCTTCCAGGTCAAGTGGATTATGCCAGGCAATA
 TTGACTGCAGAGCTGAAGGGACACCATCTCTGAAGTCATGTGGATCATGCCAGCAATA

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 TTTTCTCCAGCTCCATACTTTTGGAGCAGAGTCACGGTCCATCCAAATGGAACCTTGG
 TTTTCTCCAGCCCCATACTATGGAAGCAGAAATCACAGTCCATAAAATGGAACCTTGG

rat_cDNA
 human_5+3 corrected
 mus_cDNA_5
 AGATGAGGAACATCCGGCTTCTGACTCTGCGGACTTCACTGTGTGGTTCCGAGCGAGG
 AAATTAGGAATGTGAGGCTTTCAGATTCAGCGACTTTATCTGTGTGGCCCGAAATGAAG

00005429.042202

rat_cDNA
human 5+3 corrected
mus_cDNA_5

GAGGAGAGAGTGTGTGGTAGTGCAGTTAGAAGTCTAGAAATGCTGAGAAGAACACAT
GTGGAGAGAGCGTGTGGTAGTACAGTTAGAAGTACTGGAAATGCTGAGAAGACCGACAT

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TCAGAAACCCATTCAACGAAAAAGTCATGCCCCAGCTGGCAAGCCCGTAGCACTGAACT
TTAGAAATCCATTTAATGAAAAAATAGTTGCCAGCTGGGAAAGTCCACAGCAATTGAATT

rat_cDNA
human 5+3 corrected
mus_cDNA_5

GCTCTGTGGATGGGAACCCCACTGAAATTAOCTGGATCTTAOCTGAOGGCACACAGT
GCTCTGTGTGATGGTAACCAOCCOCTGAAATAATCTGGATTTTAOCAAATGGCACACAGT

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TTGCTAACAGAACACACAATTCCOOGTATCTGATGGCAGGCAATGGCTCTCTCATCCTTT
TTTCCAAATGGACACAAAGTTATCAGTATCTGATAGCAAGCAATGGTTCTTTTATCATT

rat_cDNA
human 5+3 corrected
mus_cDNA_5

ACAAAGCAACTGGGAACAAGTCAGGGAAGTATCGCTGTGCAGCCAGGAATAAGGTTGGCT
CTAAACAACACTGGGAGGATGCAGGAAATATCGCTGTGCAGCTAGGAATAAAGTTGGCT

rat_cDNA
human 5+3 corrected
mus_cDNA_5

ACATCGAGAAACTCATOCTGTTAGAGATTGGGCAGAAGCCAGTCATTCTGACATAOGAAC
ATATTGAGAAATTAGTCATATTAGAAATTGGCCAGAAGCCAGTTATTCTTAOCTATGCAC

rat_cDNA
human 5+3 corrected
mus_cDNA_5

CAGGGATGGTGAAGAGCGTCAGTGGGGAACCGTTATCACTGCATTGTGTCTGATGGGA
CAGGGACAGTAAAGGCCATCAGTGGAGAATCTCTATCACTGCATTGTGTCTGATGGAA

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TCCCCAAGCCAAATGTCHAGTGGACTACACCGGGTGGCCATGTAATOGACAGGCTCAAG
TCCCTAAGCCAAATATCAATGGACTATGCCAAGTGGTTATGTAGTAGACAGGCTCAAA

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TGGATGGAAATACATACTGCATGAAATGGCAOCTGGTCATCAAAGCAACAACAGCTC
TTAATGGGAAATACATATTGCATGACATGGCACCCTTAGTCATTAAAGAGCAACAGCTT

rat_cDNA
human 5+3 corrected
mus_cDNA_5

ACGAACAGGAAATATATCTGTAGGGCTCAAAACAGTGTGGCCAGGCAATTATTAGCG
ATGACAGAGGAACTATATCTGTAAGGCTCAAAATAGTGTGGTCATACACTGATTACTG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TGTCAGTGATGGTGTGGCTACCTCCCCGAATCATAAACTAOCCTAACAGGAACATGC
TTCCAGTAATGATGTAGCCTACCTCCCCGAATTACAAATGCTOCACCCAGGAGTATTG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

TCAGGAGGACAGGGGAAGCCATGCAGCTCCACTGTGTGGCCTTGGGAATCCCCAAGCCAA
TCACCAGGACAGGGGCAGCCTTTCAGCTCCACTGTGTGGCCTTGGGAGTTCCCAAGCCAG

rat_cDNA
human 5+3 corrected
mus_cDNA_5

AAGTCAOCTGGGAGACGCCAAGACACTOCTGCTCTCAAAGCAACAGCAAGAAACCCC
AAATCACATGGGAGATGCTGAOCCACTOCTTCTCTCAAAGCAAGTAAAGAGAGGACAC

rat_cDNA
human 5+3 corrected
mus_cDNA_5

ATAGAAGTGAGATGCTTCACCCACAAGGTACGCTGGTCATTGAGAAATCTCCAAACCTGG
ATGGAAGTGAGCAGCTTCACTTACAAGGTACCTAGTCATTGAGAAATCCCCAACTCCG

20220706 02:50:00

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ATTCTGGGATATACAAATGCACAGCAAAGAACCCACTTGGTAGTGATTATGCAGCAAGCT

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ATATTCAAGTAATCTGACATGAA-----ATAATAAAGT-CAACAA-----CATCTGGGCA

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GCATTATGAAGTGAATGATACTGATTATTTAATGGATCTCAAAGCAAAGCTTTTAACTTAA

GGCACTTTGATTTTGGCAACAAATAATAACAAACATTAAGAGAAAAAATGATCCACTAC
GGCACTTTTATTTTGGCAACAAATAACAATAAACAA----ACATTGAAACGGTTCATAT

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AAAATAACAAATGGCTAATGTACCTGAATTTTTTCAGTAAAAAAA--TGAAGTT-CTAAT

AGTTGCCAGCTGCCTCGTGTCTGTTTCCTACCAATGTCAACAACATCGCACACAGGGTGA
A---CCAGTTGCCTAGTGTCCACCTCCATCAATGTTACAAGCATGGCACTCAG---A

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ACAGAGACATGGAATAATTAAATCTGC-----AATCT--ATGTATAAATATTT

TGTGNCCTGGTTTATAAACATTTT-GATAAACCAGAAAAA
TGT---GGTTTATAAATTTTTTGTCTAAAACTACAGAAATAG

AAAA

(rat_cDNA: SEQ ID NO:7)
(human_5+3 corrected: SEQ ID NO:8)
(mus cDNA_5: SEQ ID NO:9)

[illegible]

rat
human_5+3_corrected
mouse_5_corrected

MQVRGREVSGLLISLTAVCLVVT PGSRACPRRCACYPTVEHCTFRYLTSIPDGIPANVE
MKVKGRGITCLLVSVFAVICLVATPGGKACPRRCACYMTEVHCTFRYLTSIPDSIPPNVE
MQKRGREVSCLLISLTATCLVVT PGSRVCFRRACAYPTEVHCTFRDLTSPD-GPANVE

rat
human_5+3_corrected
mouse_5_corrected

RINLGYNLSRLTLTENDFDGLSKLELLMLHSNGIHRVSDKTFSGQLSQVLKMSYNKVQII
RINLGYNLSVRLMETDFSGLTLELLMLHSNGIHTIPDKTFSDLOALQVLKMSYNKVRKL
RVNLGYNSLTRLTENDFSGLSKLELLMLHSNGIHRVSDKTFSGQLSQVLKMSYNKVQII

rat
human_5+3_corrected
mouse_5_corrected

RKDTFYGLGSVLRLHLHDNNIEFINPEAFYGLTSLRLVHLEGNRLTKLHPDTFVSLSYLQ
QKDTFYGLRSLTRLHMDHNNIEFINPEVFYGLNFLRLVHLEGNQLTKLHPDTFVSLSYLQ
EKDTLYGLRSLTRLHLDHNNIEFINPEAFYGLTLLRLVHLEGNRLTKLHPDTFVSLSYLQ

rat
human_5+3_corrected
mouse_5_corrected

IFKTSFIKYLELSDNF LTSLPKEMVSYMPNLESYLHGNEFTCDCHLKWLSEWMOGNPDI
IFKISFIKFLYLSDNFLTSLPLQEMVSYMPDLDSL YLHGNEFTCDCHLKWLSDWIQ--PDV
IFKTSFIKXLYLYDNF-TSLPKEMVSSMPNLESYLHGNEFTCDCHLKWLSEWMGNP---

rat
human_5+3_corrected
mouse_5_corrected

IKCKKDRSSSSPOQCPLMNPRI SKGRPFAMVP SGAF LCTKPTIDPSLKS KSLVTOEDNG
IKCKKDRSPSSAQOQCPLCMNPRT SKGKPLAMVSAARAFCAKPTIDS SLKS KSLTILEDSS

rat
human_5+3_corrected
mouse_5_corrected

SASTSPQDFIEPFGSLSLNMTXXSGNKADMVCS IQKFSRTSPTA TEENDYTMINASFSST
SAFISPOGFMAFPFGLTIAMTDQSGNEARMVCS IQKFSRTSPIA TEENDYIVLNTSFSST

rat
human_5+3_corrected
mouse_5_corrected

NLVCSDVDYNIHQPVWQILALY8DSPLILERKPQTETPSLSRYKQVALRPEDIFT SIEA
FLVCNIDYGHIQPVWQILALY8DSPLILERSHLLSETPOLYKYKQVAPKPEDIFTNIEA

rat
human_5+3_corrected
mouse_5_corrected

DVRADPFWFQQEKIVLQINRTATTTLSTLQIQFSTDAQIALPRAENRAERLKWTMIIMMN
DIRADPSWLMQDQISLQINRTATTFTSLQIQYSSDAQITLPRAENRFVKHWMTI SRDN

rat
human_5+3_corrected
mouse_5_corrected

PRLERTVLVGSTIALSCPGKGDPSPHLENLIADGSKVRAPYVSEDGRILLIDKNKGLELM
TKLEHTVLVGGTGVLNCPGQGDP TPHVWLLADGSKVRAPYVSEDGRILLIDKSGKLELM

rat
human_5+3_corrected
mouse_5_corrected

ADSFDAGLYHCISTNDADADVLTIRITVVEPYGESTHDSGVQHVTVTGETL DLPCLSTGV
ADSFDTGVIHCISSNYDDADILTIRITVVEPLVEAYOENG IHTVFI GETL DLPCHSTGI

rat
human_5+3_corrected
mouse_5_corrected

PDISISWILPGNVTVFSQP SRDQITLNGTILRLIQVTFKDQGHYCVAANPSGADFSSFKV
PDASISWVIPGNVLYQSSRDKKVLNNGTILRLIQVTFKDQGYTRCVAANPSGVDFLIFV

rat
human_5+3_corrected
mouse_5_corrected

SVQKKQRNV EHDREAGSG LGEPNS SVSLKQ PASLKL SASALT GSEAG QVSGVHRKNK
SVKMKQRPLEHDGETEGSGLDES NPIAH LKEPPGAQLRTSALMEAEVGHKTSSTSKRNH

rat
human_5+3_corrected
mouse_5_corrected

HRLDIHRRRGDSTLRFRFREHRRQLPLSARRIDPORWAALLEKAKKN6VPKQENTTVKPV
YRELTLQRRGDSTHRRFRFENRRHFPPSARRIDPORWAALLEKAKKNAMPKRENTTVSFP

```

rat      WPEHKYQLKSYSETIEKGRPAVSMSPHLSLPEASTHASHWNTQKHAESKSVFDKKPGQNPF
human_5+3_corrected WAELYQFWHKPYSDLAERKGGKPEVSMATTGLSEATTIVSDWDGQKNTKKSDFDKKPQDEA
mouse_5_corrected -----

```

rat -TSKHLPYVSLPKTLKPKRIIGGKAASFTVPANSDFVLPCEAVGDLPIIHWTRVSSGX
 human_5+3_corrected TTSKLLPFDLSRYIFEKPRIVGGKAASFTIPANSDAFLPCEAVGNPLPTIHWTRVS-GL
 mouse_5_corrected -----

rat EISQGTQKSRPHVLPNGTLSIQRVSIQDRGQYLCSAFNPLGVDHFVLSVVFYPARILD
 human_5+3_corrected DLSRGNQNSRVQVLPNGTLSIQRVSIQDRGQYLCSASNLFQTDHLHVTLVSVSYPPRIIE
 mouse_5_corrected -----

rat RHVKEITVHFGSTVELKCRVEGMPRTVSWILANQTVVSETAKGSRKVVVTPDGTLLIYN
 human_5+3_corrected RRTKEITVHSGSTVELKCRACGRPSPTVTWILANQTVVSESQGSRAVVTVDGTLVLHN
 mouse_5_corrected -----

rat LSLYDRGFYKCVASNPGGQDSLIVKIQVITAPPVILEQKROAIVGVLGSSKLPLCTAKGT
 human_5+3_corrected LSIYDRGFYKCVASNPGGQDSLIVKIQVIAAPPVILEQRRQVIVGTWGESKLPLCTAKGT
 mouse_5_corrected -----

rat PQPSVHWVLYDGTTELKPLQLTHSRFFLYPMGTLYIRSIAPSVRGITYCIATSSSGSERRV
 human_5+3_corrected PQPSVYVVLSDGTEVKELQFTNSKLFLFSNGTLYIRNLASSDRGTYECIATSSSGSERRV
 mouse_5_corrected -----

rat VILTVEEGETIPRIETASQKWEVNLGEKLLNCSATGDPKPRIIWRLPKKAVIDQWHRM
 human_5+3_corrected VMLTMEERVTSPIEASQKRTVNFQDALLNCSATGEPKPQIMWRLPKKAVIDQ----
 mouse_5_corrected -----

rat GSRHIVYPNGSLVVGSVTEKDGQYLCVARNKMGDDLILMHVRLRLTPAKIEQKQYFRKQ
 human_5+3_corrected GSWIHVYPNGSLFIGSVTEKDSGVYLCVARNKMGDDLILMHVSLRLPKPAKIDKQYFRKQ
 mouse_5_corrected -----

rat VLGKDFQVDCRAGSPVPEVSWSLPDGTVLNNVAQADDSGYRTKRYTLFHNGLTYFNNV
 human_5+3_corrected VLGKDFQVDCRAGSPVPEISWSLPGDTNINNAMQADDSGHRTRRYTLFNNGLTYFNKY
 mouse_5_corrected -----

rat GMAEEDGYTCSAQNTLGKDEMKVHLTVLTAIPRIQSYKTMRLRAGETAVIDLCEVTGEP
 human_5+3_corrected GVAEEDGYTCTAQNTLGKDEMKVHLTVITAAPRIQSNKTKRIKAGDTAVLDCEVTGDP
 mouse_5_corrected -----

rat KPNVFWLLPSNNVISFSNDRFTFAKRTLSTHKVKPLDSGDYVCVAQNPSGDDTKYKLD
 human_5+3_corrected KPKLFWLLPSNDMISFSIDRYTFHANGSLTINKVKLLSGEYVCVARNPSGDDTKMYKLD
 mouse_5_corrected -----

rat IVSKPPLINGLYANKTVIKATAIPHSKKYFDCRADGIPSSQVWIMPNGNIFLPAPYFGSR
 human_5+3_corrected VVSKPPLINGLYTNRTVIKATAVHRSHKHFDCAEGTPSPVWIMPONIFLTAPYFGSR
 mouse_5_corrected -----

rat VTVHPNGTLEMRNIRLSDSADFTCVVRSEGGE5VLVVQLEVLMLRRPTFRNPFNEKIVA
 human_5+3_corrected ITVHKNGTLEIRNVRLSDSADFTCVARNEGGESVLVVQLEVLMLRRPTFRNPFNEKIVA
 mouse_5_corrected -----

rat QAGKPVALNCSVDGNPPPEITWILPDGTQFANRPANSPYLMAGNGSLILYKATRNK9GKY
 human_5+3_corrected QLGKSTALNCSVDGNPPPEIIWILPNGTRFSNGPQSYQYLIASNGSFIISKTTREDAGKY
 mouse_5_corrected -----

rat RCAARNKVGYTEKLILLEIGQKPVILTYEPGMVKSVSGEPLSLHCVSDGIPKPNVKTTP
 human_5+3_corrected RCAARNKVGYTEKLVILEIGQKPVILTYAPGTVKSIGESLSLHCVSDGIEKPNIKWTMP
 mouse_5_corrected -----

00005420-01200

rat GGHVIDRPQVDGKYILHENGTLVIKATTAHDQGNVICRAQNSVGQAVISVSVMVVAIFPK
human_5+3_corrected SGYVVDRPQINGKYILHDNGTLVIKEATAYDRGNVICRAQNSVGETLITVPVMIVAYPPR
mouse_5_corrected -----

rat IINYLFRNNLRRTGRANQLHCVALGIPKPKVTWETPRESLSKATARKPRSEMLHPQGT
human_5+3_corrected ITNRPPRSIVTRTGAAPQLHCVALGVFKPEITWEMPDHSILLSTASKERTHGSEQLHLQGT
mouse_5_corrected -----

rat LVIQNLQTSDSGVYKCRANLLGTDYATYIQV
human_5+3_corrected LVIQNPQTSDSGIYKCTAKNPLGSDYAATYIQV
mouse_5_corrected -----

(rat: SEQ ID NO:10)

(human_5+3_corrected: SEQ ID NO:11)

(mouse_5_corrected: SEQ ID NO:12)

00005120:012200

[illegible]

[illegible]

rat
 human_5+3_corrected
 SRIHVYPNGSLVVGSVTERKAGDYLCVARNKNGDOLVIMHVRLRLTPAKIBQKQYFKKQV
 SWIHVYPNGSLFIGSVTERKSGVYLCVARNKNGDOLIMHVSLRLPKAKIDHKQYFRKQV
 * *****,*:*****;* *****,*:*****:**** **,*:*****:****:****:****

rat
 human_5+3_corrected
 LHGKDFQVDCASGSPVPEVSWSLPDGTVLNNVAQADDSGYRTKRYTLFENGTLYPNNVG
 LHGKDFQVDCASGSPVPEISWSLDPGTMNNAMQADDSGHRTRRYTLFNNGTLYFNKVG
 *****,*:*****:*****,*:*****:*****,*:*****:*****,*:*****:****

rat
 human_5+3_corrected
 MAEGDYICSAQNTLGKDEKRVHLTVLTAIPRIQSYKTMLRAGETAVLDCEVTGEPK
 VAEEDYTCAQNTLGKDEKRVHLTVITAAPRIQSNKTKRIKAGDTAVLDCEVTGDEK
 *,***** * *****,*:*****:*****,*:*****:*****,*:*****:****

rat
 human_5+3_corrected
 PNVFWLLPSMNVISFSNDRFTFHANRTLSIHKVKPLDSGDYVCVAQNPSGDDTKTYKLDI
 PKIFWLLPSNDMISFSDRYTFHANGSLINKVLLDSGEYVCVARNPSGDDTKMYKLDV
 *,*****:*****,*:*****:*****,*:*****:*****,*:*****:****

rat
 human_5+3_corrected
 VSKPPLINGLYANKTVIKATAIRHSKKYFDCRADGIPSSQVTWIMPNIPLPAPYFGRV
 VSKPPLINGLYTNRTVIKATAVRHSKRHEDCRAEGTPSPVEMWINEPDNIFLTAPYTGRI
 *****,*:*****:*****,*:*****:*****,*:*****:****

rat
 human_5+3_corrected
 TVHPNGTLEMRNIRLSDSADFTCVVRSEGGESVLVVQLEVLMLRPTFNPFFNEKIVAQ
 TVHKNGTLEIRNVRLSDSADFTCVARNEGGESVLVVQLEVLMLRPTFNPFFNEKIVAQ
 ,*:**:*****,*:*****:*****,*:*****:****

rat
 human_5+3_corrected
 AGKPVALNCSVDGNPPPEITWILPDGTQFANRPHNSFYLMAGNGSLILYKATRNKSGKYR
 LGKSTALNCSVDGNPPPEITWILPNGTRFSNGPQSYQLIASNGSEFIISKTTREDAGKYR
 ,*:***:*****,*:*****:*****,*:*****:****

rat
 human_5+3_corrected
 CAARNKVGYIEKLILLEIGQKPVILTYEPMVKSVSCEPLSLHCVSDGIPKPNVKWTPG
 CAARNKVGYIEKLIVILEIGQKPVILTYAPGTVKGISGESLSLHCVSDGIPKPNIKWTMPS
 *****,*:*****:*****,*:*****:*****,*:*****:****

rat
 human_5+3_corrected
 GHVIDRPQVDGKYILHENGTLVIKATTAHQGNVICRAQNSVGQAVISVSMVVAIPPRI
 GVVDRPQINGKYILHDNGTLVIKATAYDRGNVICRAQNSVGHTLITVPMIVAIIPPRI
 ,:*****:*****,*:*****:*****,*:*****:****

rat
 human_5+3_corrected
 INYLPNNMLRRTGEANQLHCVLGIKPKVTVETPRHSLLSKATARKPHRSEMHPQGTIL
 TNAPPRIIVTRTGAATQLHCVLGVKPEITWEMPDSHLLSTASKERTHGSEQLHLQGTIL
 * **,*: **** *,*:*****:*****,*:*****:****

rat
 human_5+3_corrected
 VIONLQTSDSGVYKCAQNLLGTDYATYIQVL
 VIONPQTSDSGIYKCTARNPLGSDYATYIQVI
 **** *,*:*****:*****,*:*****:****

(rat: SEQ ID NO:13)

(human_5+3_corrected: SEQ ID NO:14)

Figure 17

MQKRGREVSCLLISLTAICLVVTPGSRVCPRRACACYVPTEVHCTFRDLTSIPDGPANVER
 VNLGYNSLTRLTENDFSGLSRLELLMLHSNGIHRVSDKTFSGLSLQVLKMSYNKVQIE
 KDTLYGLRSLTRLHLDHNNIEFINPEAFYGLTLLRLVHLEGNRLTKLHPDTFVSLSYLQIF
 KTSFIKXLYLYDNFTSLPKEMVSSMPNLESYLHGNPWTCDCHLKWLSEWMQGNP
 (SEQ ID NO: 15)

Figure 18

MKVKGRGITCLLVSFAVICLVATPGGKACPRRCACYMPTEVHCTFRYLTSSIPDSIPPNVE
 RINLGYNLSLRLMETDFSGLTKELELLMLHSNGIHTIPDKTFSDLQALQVLKMSYNKVRK
 LQKDTFYGLRSLTRLHMDHNNIEFINPEVFYGLNFLRLVHLEGNQLTKLHPDTFVSLSYL
 QIFKISFIKFLYLSDNFTSLPQEMSYPDLDSLLYLHGNPWTCDCHLRWLSDWIQPDVI
 KCKKDRSPSSAQQCPLCMNPRTSKGKPLAMVSAAAFQCAKPTIDSSLKSKSLTILEDSSS
 AFISPOGFMAPFGSLTLNMTDQSGNEANMVCSIQKPSRTSPIAFTEENDYIVLNTSFSTFL
 VCNIDYGHIQPVWQILALYSDSPLILERSHLLSETPQLYYKYKQVAPKPEDIFTNIEADLR
 ADPSWLMQDQISLQLNRTATTFTLQIQYSSDAQITLPRAEVRPVKHKWTMISRDNNTK
 LEHTVLVGGTVGLNCPGQGDPTPHVDWLLADGSKVRAPYVSEDGRILIDKSGKLELQM
 ADSFDTGVYHCISSNYDDADILTYRITVVEPLVEAYQENGIHHTVFIGETLDLPCHSTGIP
 DASISWVIPGNNVLYQSSRDKKVLNNGTLRLQVTPKDQGYRCVAANPSGVDFLIFQV
 SVKMKGQRPLEHGETEGSGLDESNPIAHLKEPPGAQLRTSALMEAEVKGHTSSTSKRH
 NYRELTLQRRGDSTHRRFRENRRHFPPSARRIDPQHWAALLEKAKKNAMPDKRENTTV
 SPPPVTQLPNIPGEEDDSSGMLALHEEFMVPATKALNLPARTVTADSRTISDSPMTNIN
 YGTEFSPVNSQILPPEEPTDFKLSTAILTTAMSKNINPTMSSQIQGTTNQHSSTVFPLLLG
 ATEFQDSDQMGRGREHFQSRPPITVRTMIKDVNVKMLSSTTNKLLLESVNSHQTSVREV
 SEPRHNHFYSHTTQILSTSTFSPDPHTAAHSQFPIPRNSTVNIPLFRRFGRQRKIGGRGRIIS
 PYRTPVLRHRYSIFRSTTRGSSEKSTTAFSATVLNVTCLSLPRELTTATAALSFPASAPI
 TFPKADIARVPSEESTTLVQNPLLLLENKPSVEKTTPTIKYFRTEISQVTPTGAVMTYAPT
 SIPMEKTHKVNASYPRVSSTNEAKRDSVITSSLSGATKPPMTIATFRSRRKIPWQQNFV
 NNHNPKGRLRNQHKVSLQKSTAVMLPKTSPALPQRQSSPFHFRRLSTSVMQIPSNLTIT
 AHHTTTKTHNPGSLPTKKELPFPLNPMLPSIISKDSSTKSIISTQTAIPATPTFPASVITYE
 TQTERSRAQTIQREQEPQKKNRTPDNISPDQSSGFTTPTAMTPPALAFTHSPPENTTGISST
 ISFHSRTLNLTDVIEELAQASTQTLKSTIASSETTLSSKSHQSTTTRKASLDTPIPPFLSSSAT
 LMPVPISPPFTQRAVTDTRGDSHFRLMTNTVVKLHESSRHNLQMPSSQLEPLTSSTSNLL
 HSTPMPALTTVKSQNSKLTSPSPWAEQFWHKPYSDIAEKGGKPEVSMMLATTGLSEATTLV
 SDWDGQKNTKKSDFDKKPVQEATTSKLLPFDSLRYIFEKPRIVGGKAASFTIPANSDAF
 LPCEAVGNPLPTIHWTRVSGDLRSNGNQRSRVQVLPNGTLSIQRVEIQDRFQYLCSASNL
 FGTDHLHVTLVSVSYPRIERLRTKEITVHSGSTVELKCRAEGRPSPTVTWILANQTVVSE
 SSQGSRQAVVTVDGTLVLHNLISIYDRGFYKCVASNPGGQDSLLVKIQVIAAPPVILEQRR
 QVIVGTWGESLKLPCATAKGTPQPSVYVWVLSDGTEVKPLQFTNSKLFLFSNGTLYIRNLAS

0005120 04303
 0005120 04303

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SDRFTYECIATSSTGSERRVVMLTMEERVTSPIREAASQKRTEVNFQDKLLLNCSATGEP
KPQIMRLPSKAVVDQGSWIHYPNGSLFIGVTEKDSGVYLCVARNKMGDDLILMHVSLR
LKPAKIDHKQYFRKQVLHGKDFQVDCKASGSPVPEISWSLPDGTMINNAMQADDSGHR
TRRYRLFNNGTLYFNKVGVAEEGDYTCYAQNTLGKDEMKVHLTVITAAPRIRQSNKTN
KRIKAGDTAAVLDCEVTGDPKPKIFWLLPSNDMISFSIDRYTFHANGSLTINKVKLLDSG
EYVCVARNPSGDDTKMYKLDVVSKPPLINGLYTNRTVIKATAVRHSKKHFDCRAEGTP
SPEVMWIMPDNIFLTAPYYGSRITVHKNGTLEIRNVRLSADFICVARNEGGEVLVVQLE
VLEMLRRPTFRNPRNPFNEKIVAQLGKSTALNCVSVDGNPPPEIHWILPNGTRFSNGPQSY
QYLIASNGSFIISKTTREDAGKYRCAARNKVGYYIEKL VILEIGQKPVILTYAPGTVKGISGE
SLSLHCVSDGIPKPNIKWTMPSGYVVD RPQINGKYILHDNGTLVIKEATAYDRGNYICKA
QNSVGHTLITVPVMIVAYPPRITNRPPRSIVTRTGAAFLHCVALGVKPEITWEMPDHS
LLSTASKERTHGSEQLHLQGT LVIQNPQTSDSGIYKCTAKNPLGSDYAATYIQVI (SEQ ID
NO: 16)

Figure 19

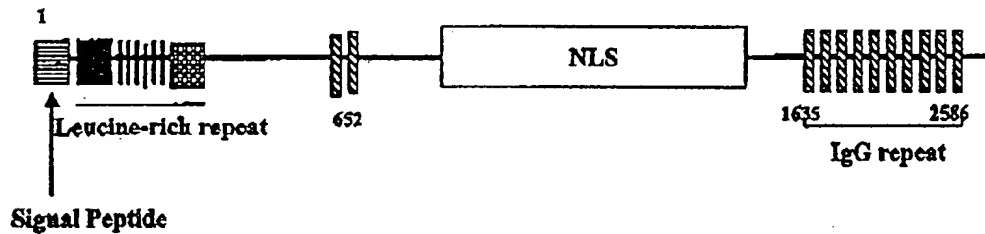


Figure 20

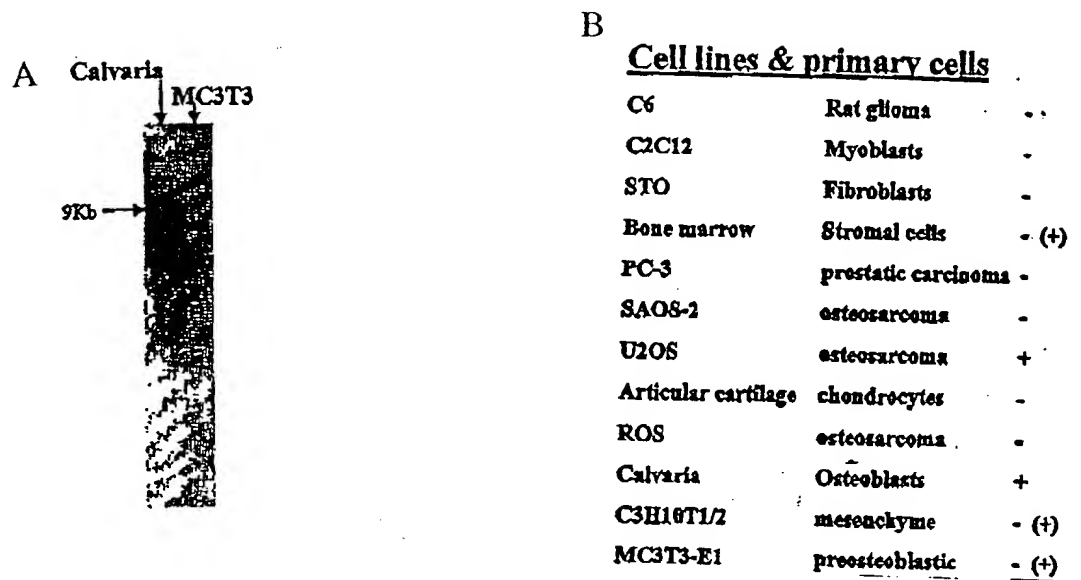
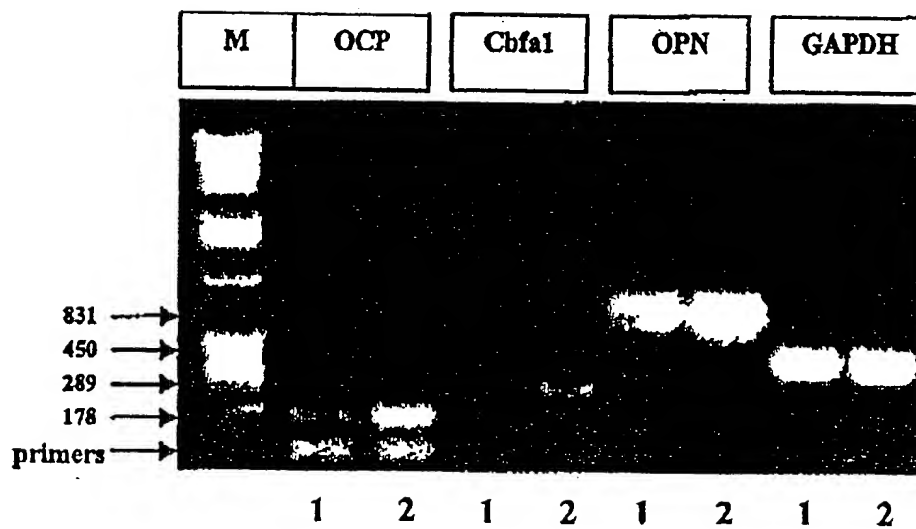


Figure 21



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Figure 22

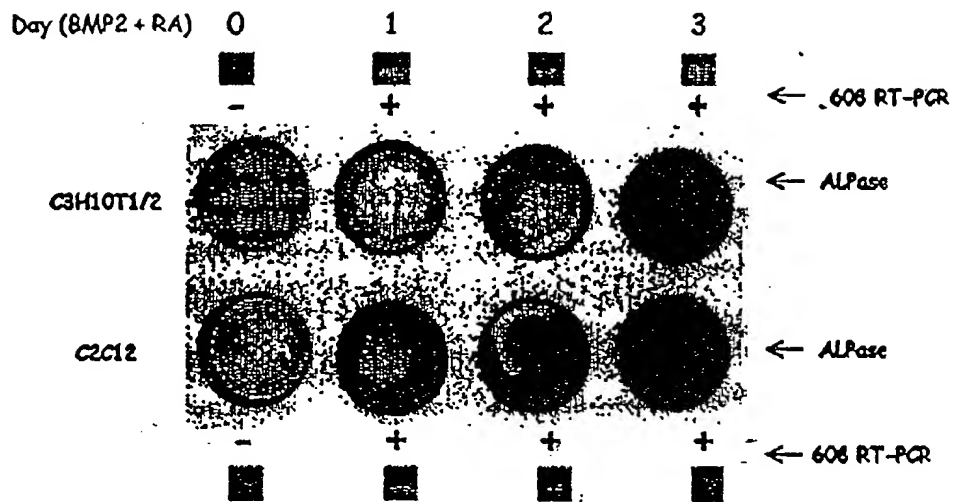
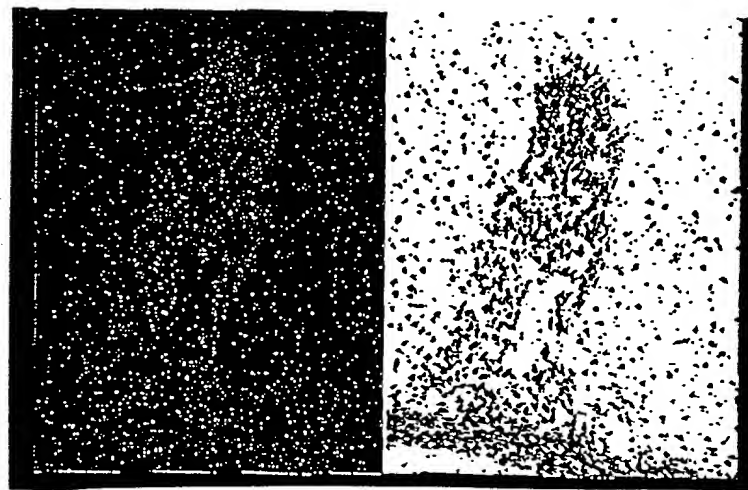


Figure 23



00005430 042203

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Figure 24

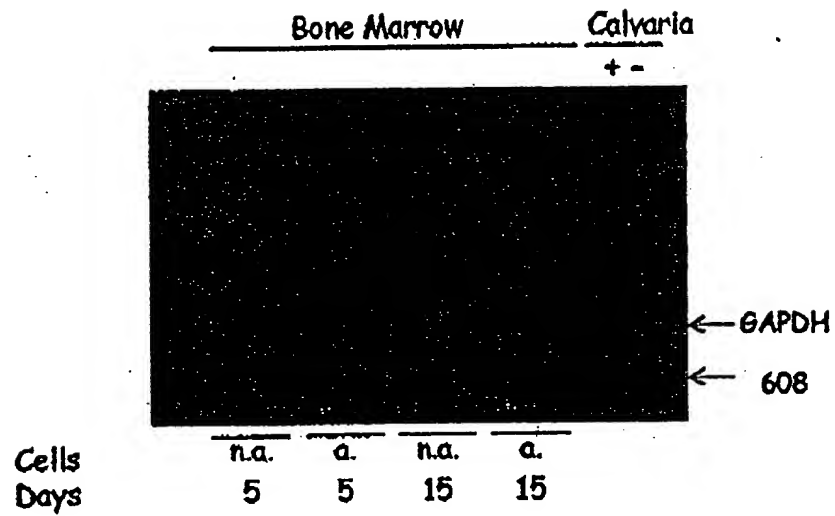
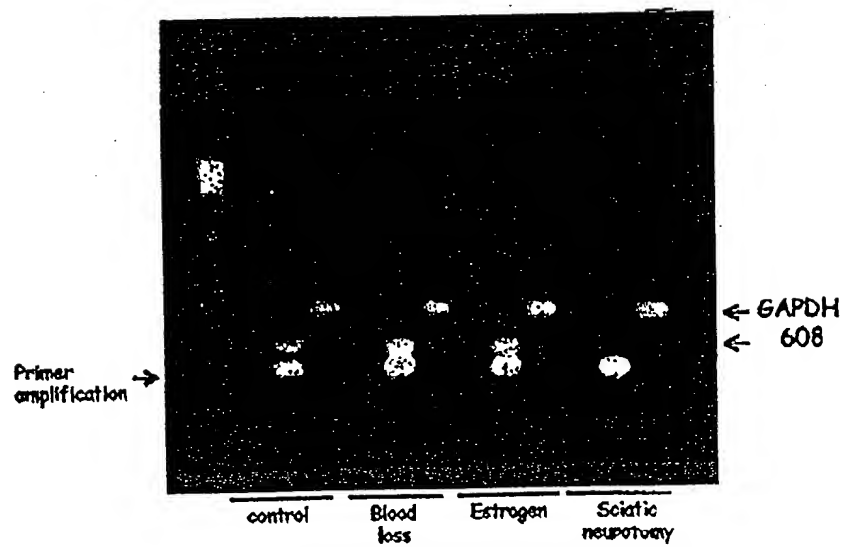
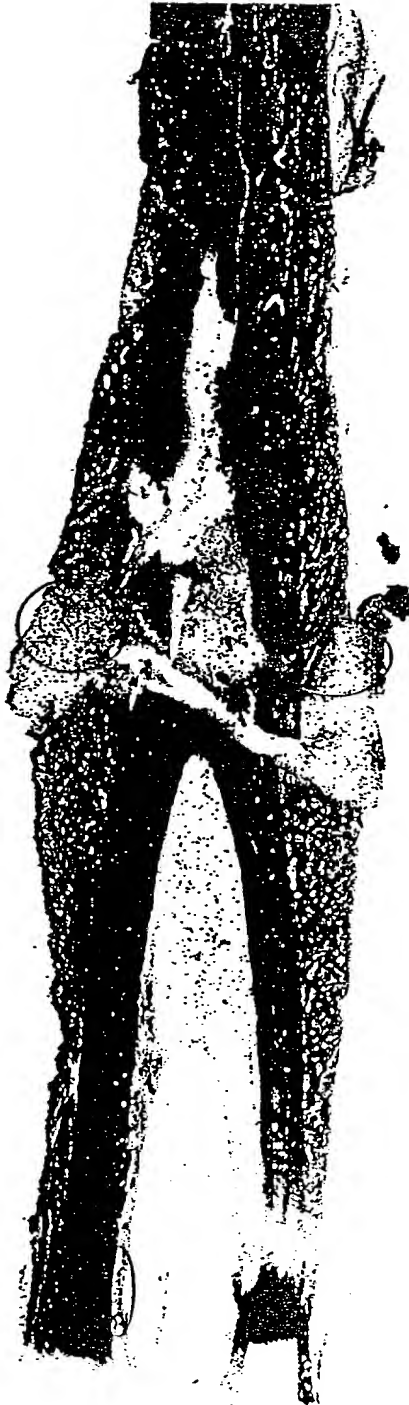


Figure 25



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Figure 26

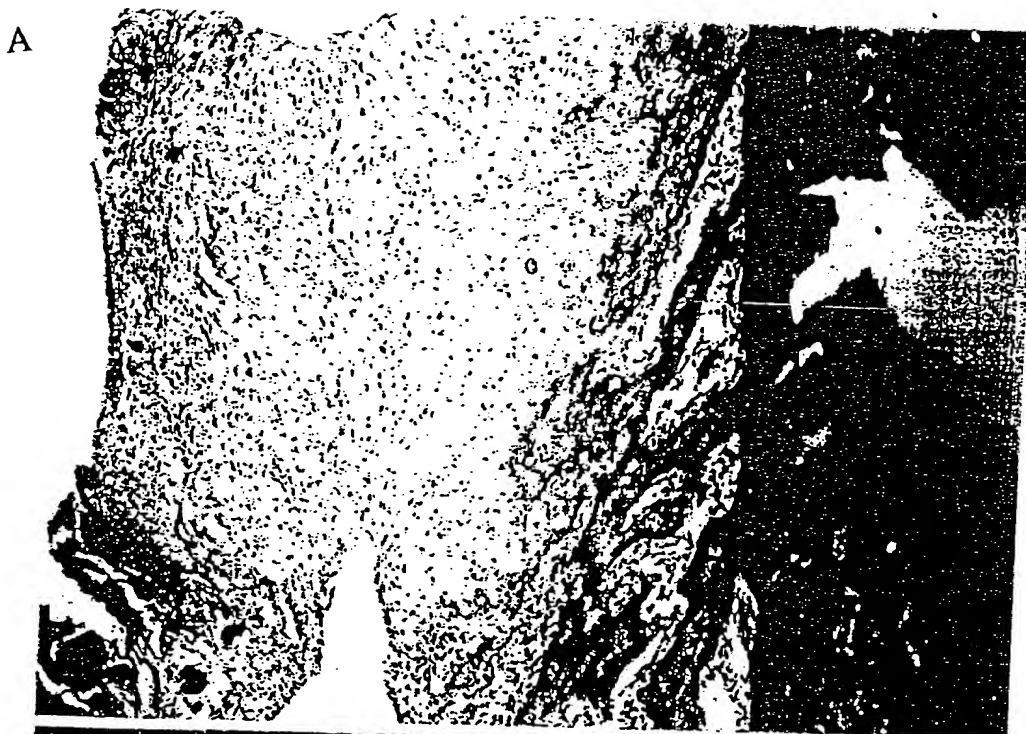


202210 0005120 042202

[illegible]

A high-contrast, black and white photograph showing a close-up of a textured surface, possibly a wall or ceiling. The surface is covered in a dense, granular pattern of small dark spots and irregularities. In the lower center, there is a bright, irregularly shaped object that appears to be a light fixture or a hole, casting a strong glow. The overall image has a grainy, high-contrast quality, typical of a photocopy or a low-quality scan.

A high-contrast, black and white image showing a dense, textured surface, possibly a wall or a large object, with a bright, irregular shape in the lower center. The image is heavily speckled and noisy, with a dark, grainy background and a bright, irregular shape in the lower center. The overall appearance is that of a low-quality, high-contrast scan or a heavily textured surface.

[illegible]

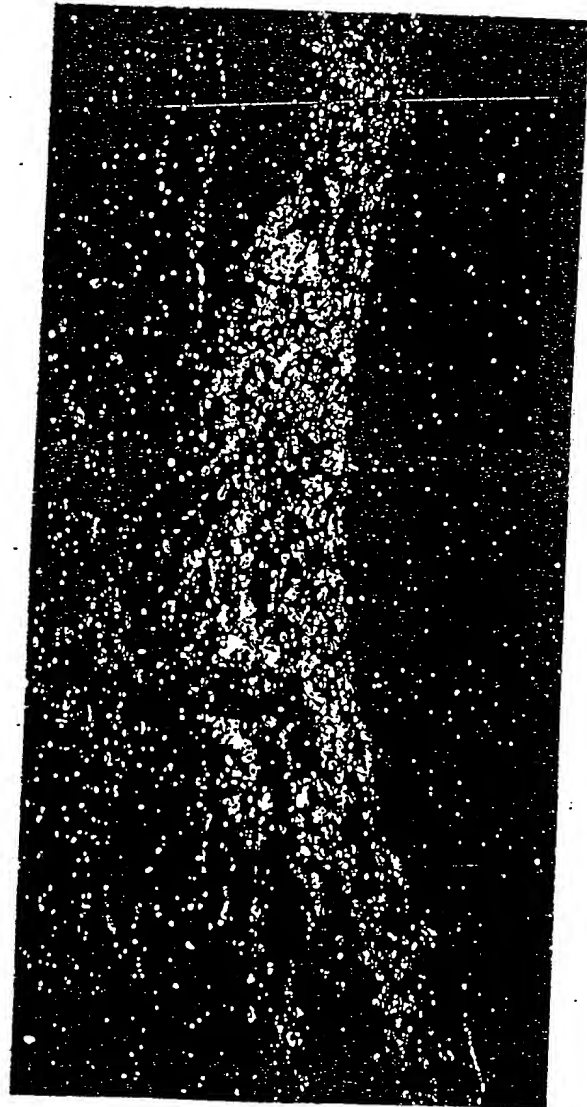
56/90

Figure 29

A



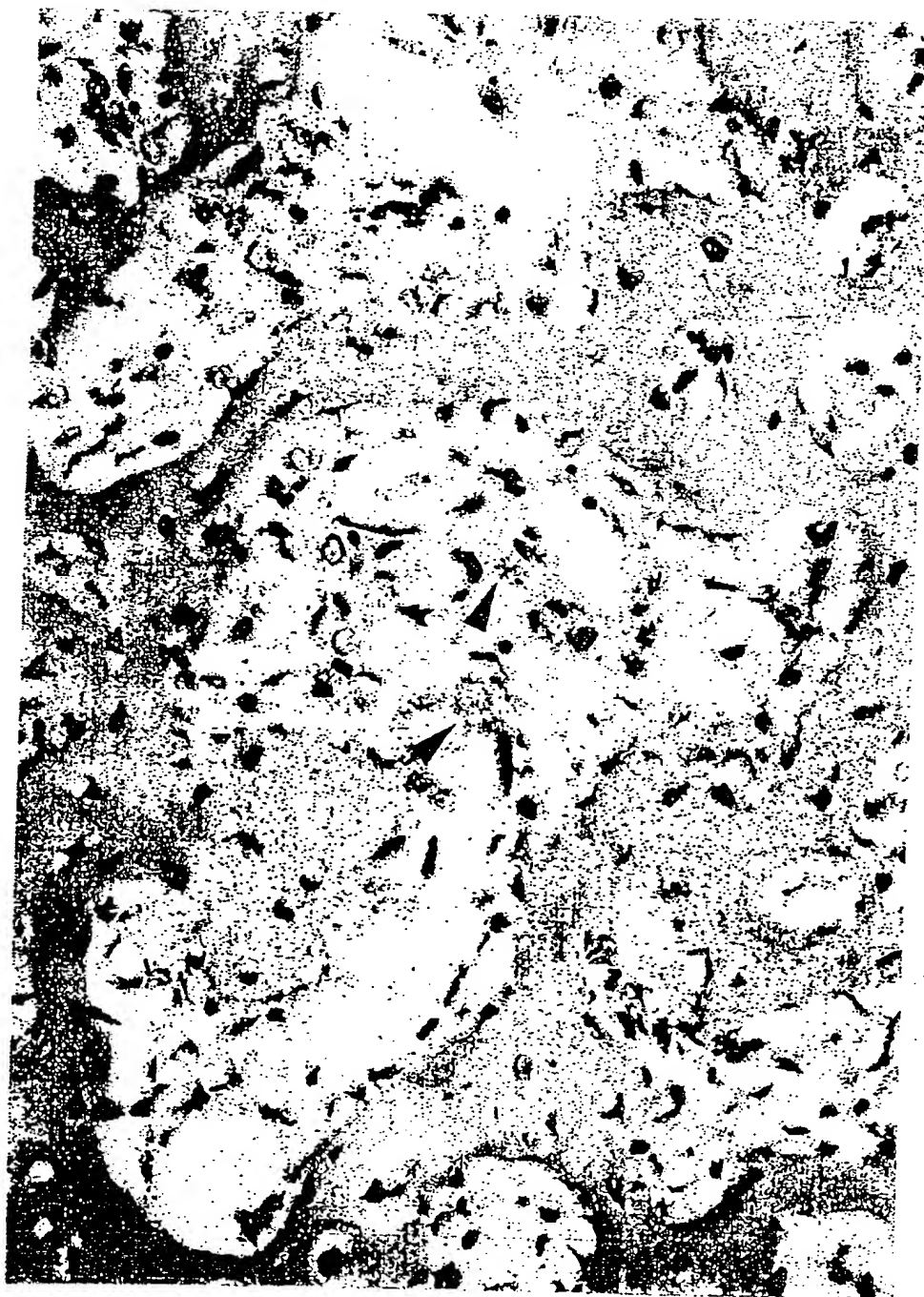
B



00005129.012202

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Figure 30



202210 02150000

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Figure 31



00005430.042002

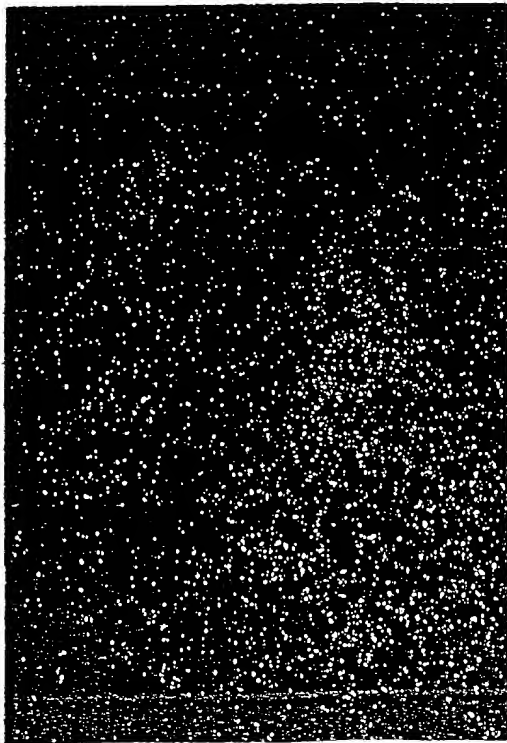
59/90

Figure 32

A



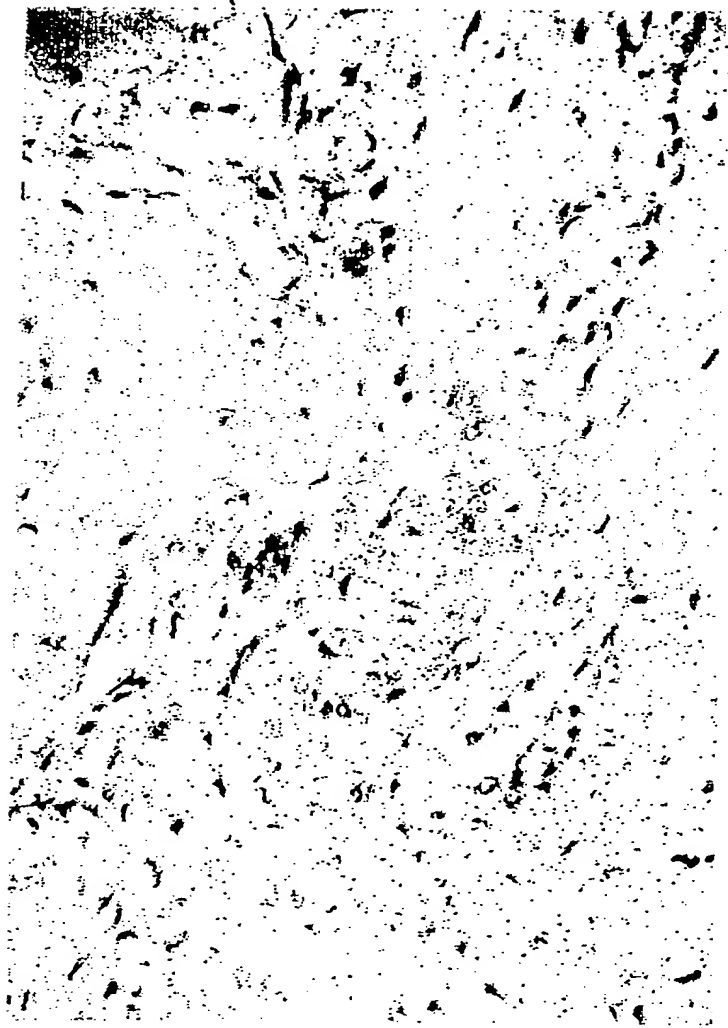
B



00005120 042202

60/90

Figure 33



00005430.042203

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Figure 34

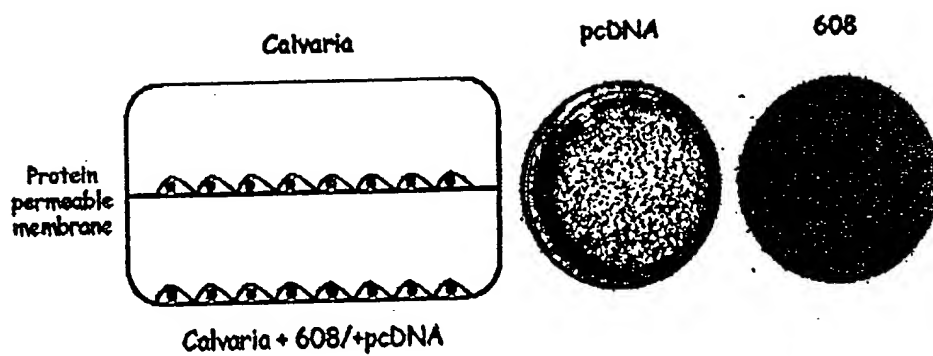
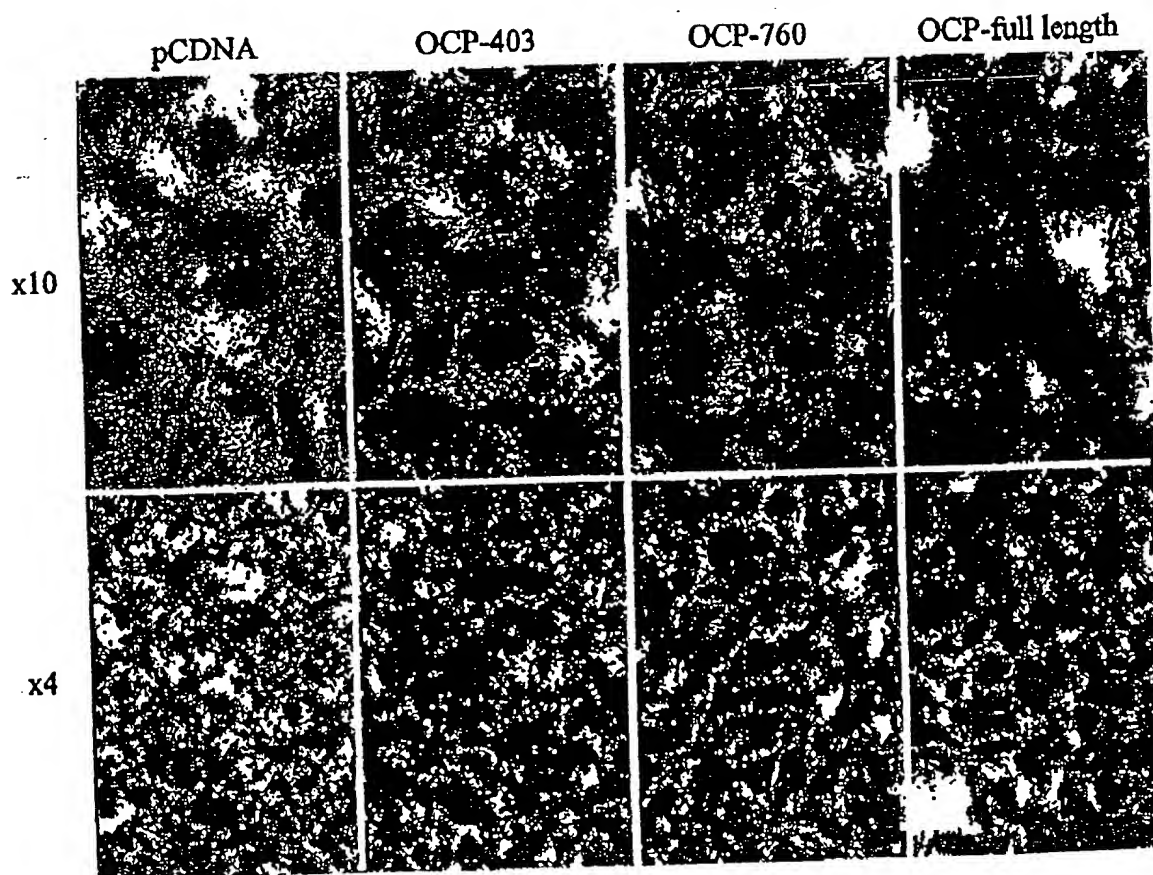


Figure 35



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Figure 36

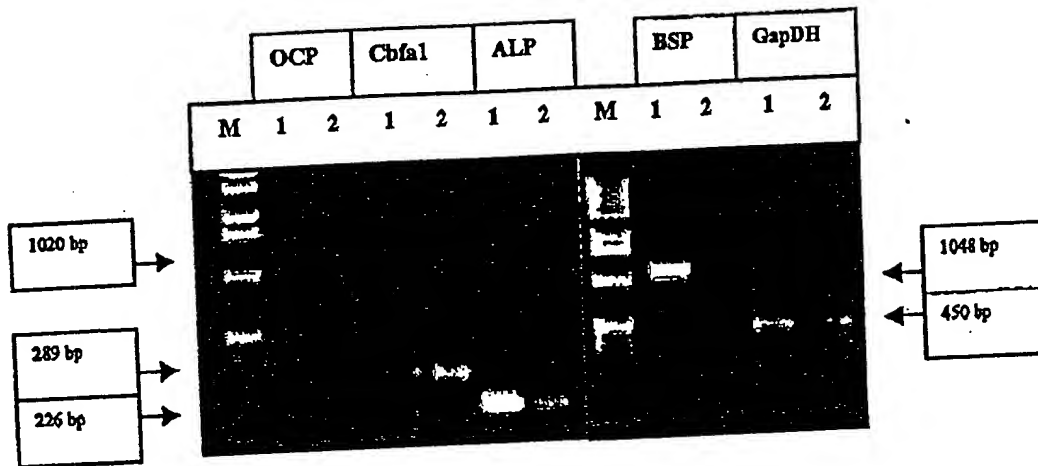


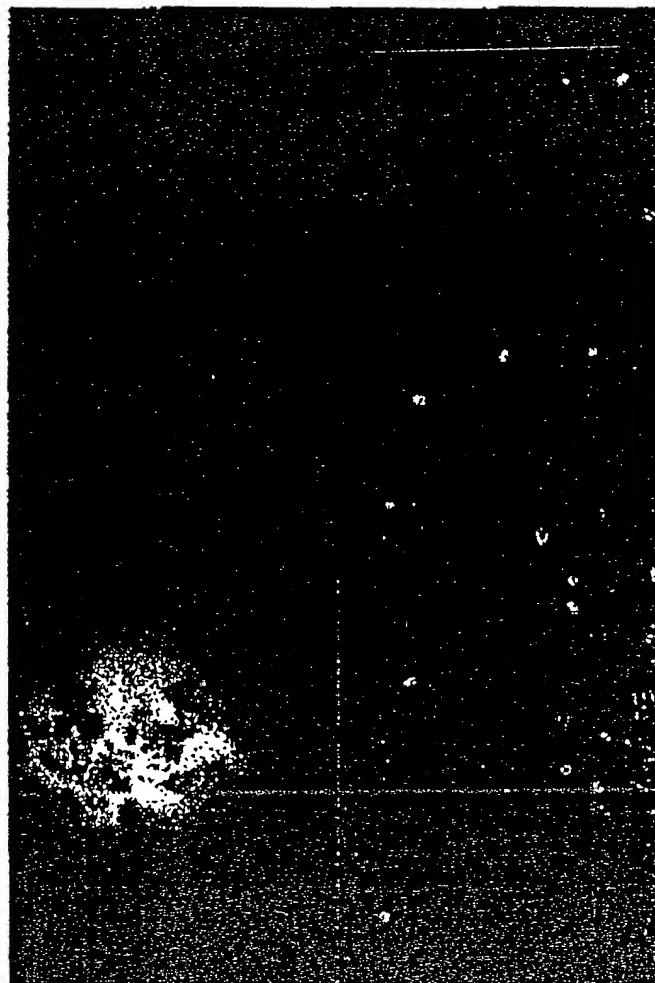
Figure 37

x 4

x 10

pCDNA
ROS stable line

OCP
ROS stable line



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Figure 38

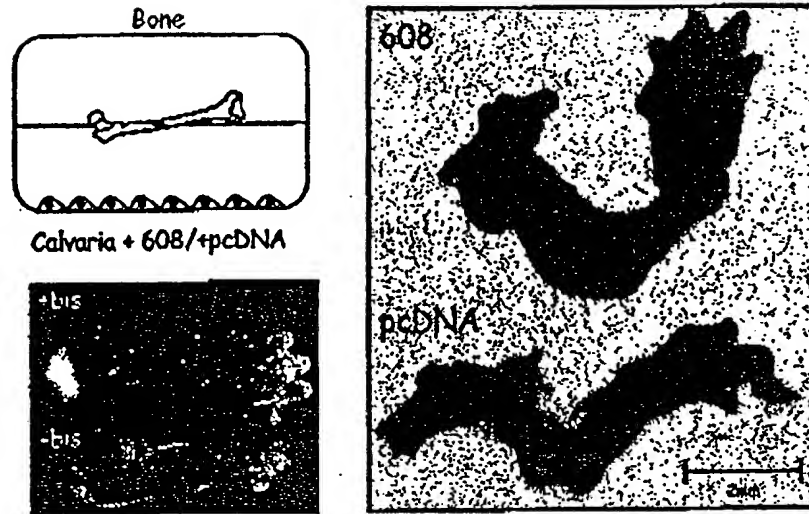
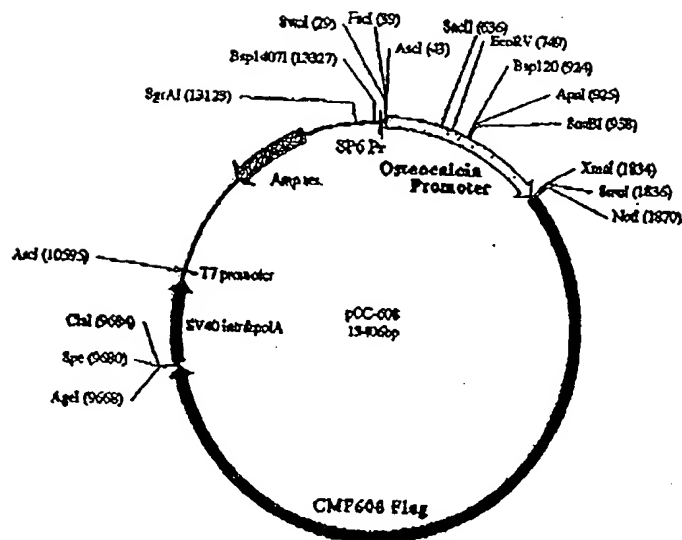
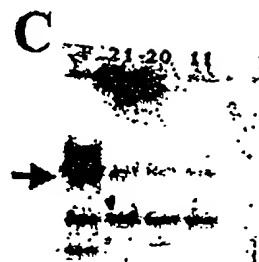
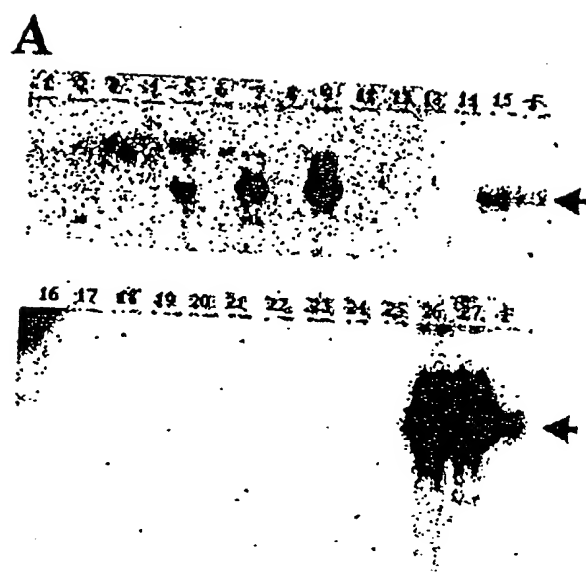


Figure 39



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Figure 40



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202210-62150000

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Figure 41

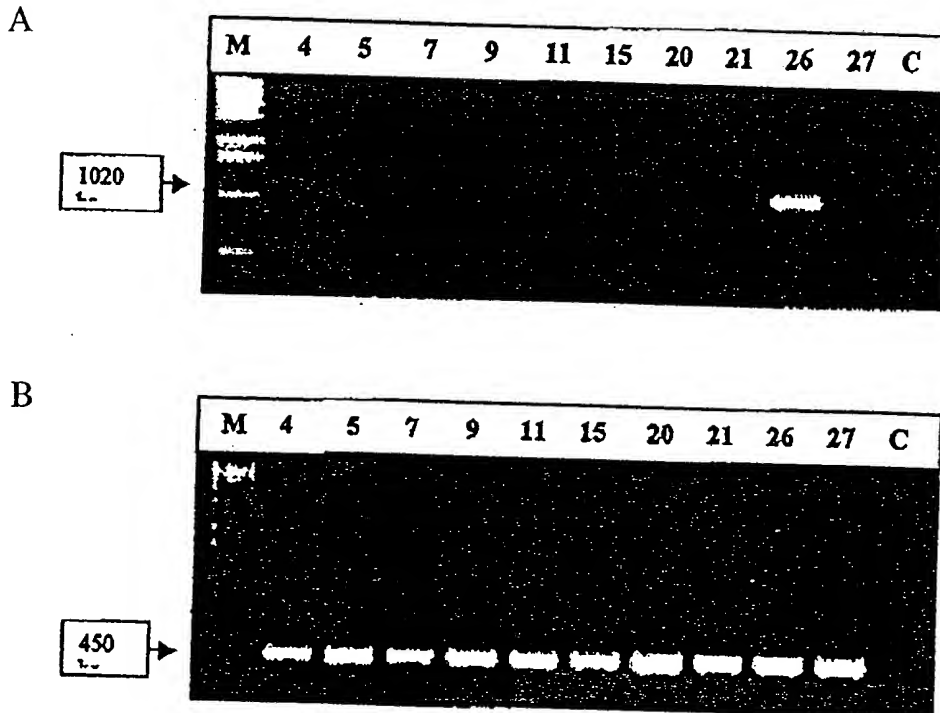
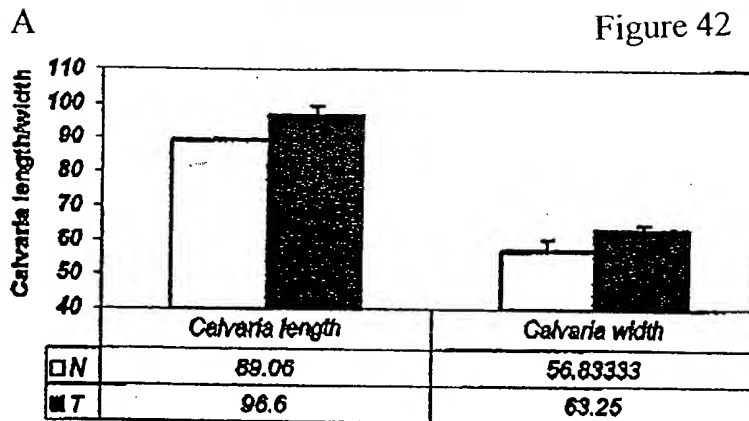
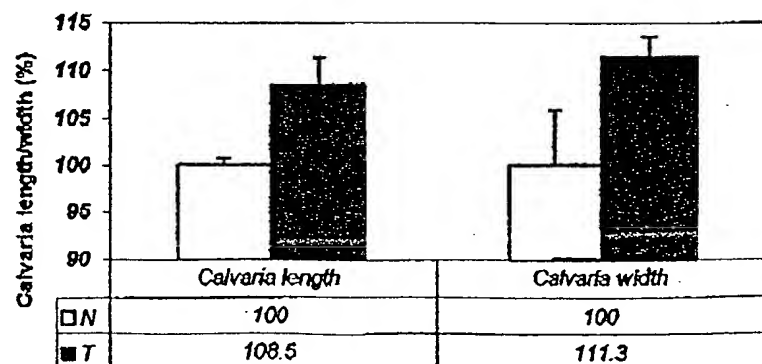


Figure 42



B



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Figure 43

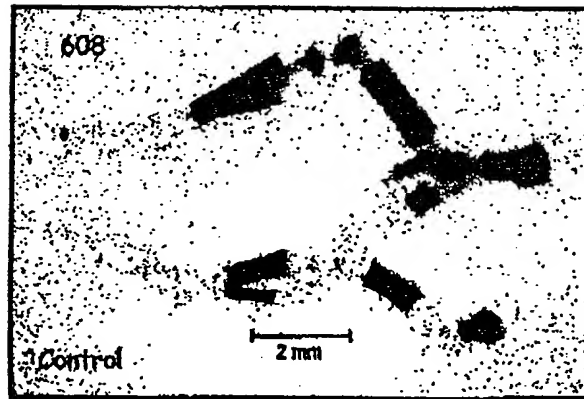
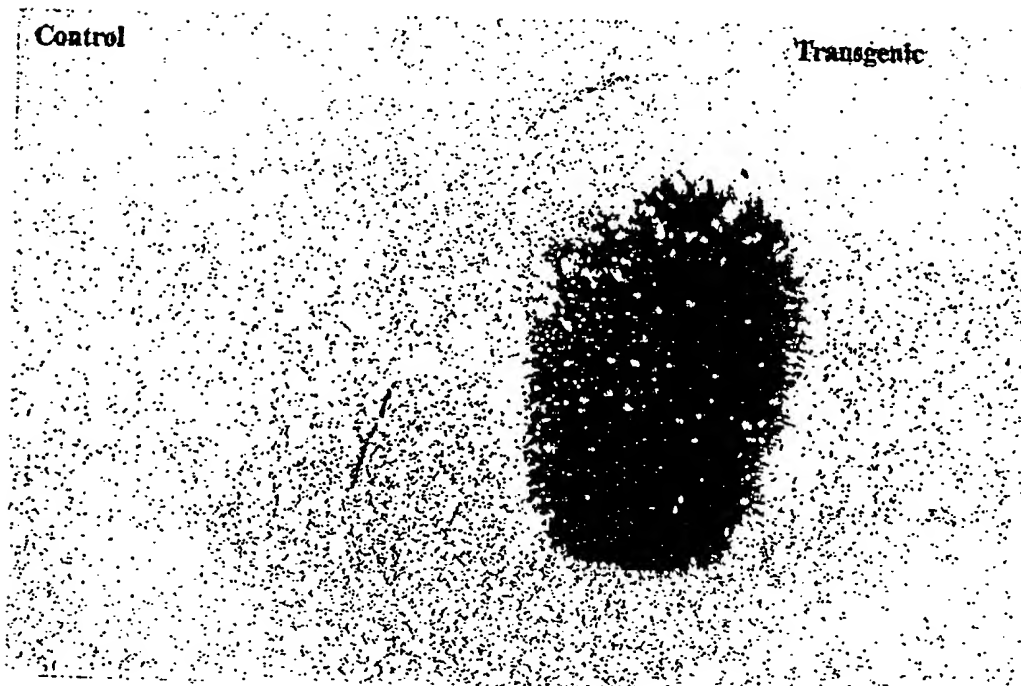


Figure 44



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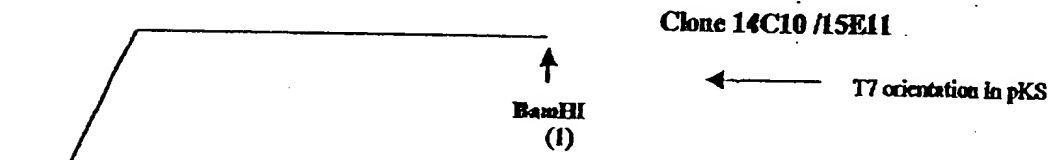
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Figure 46

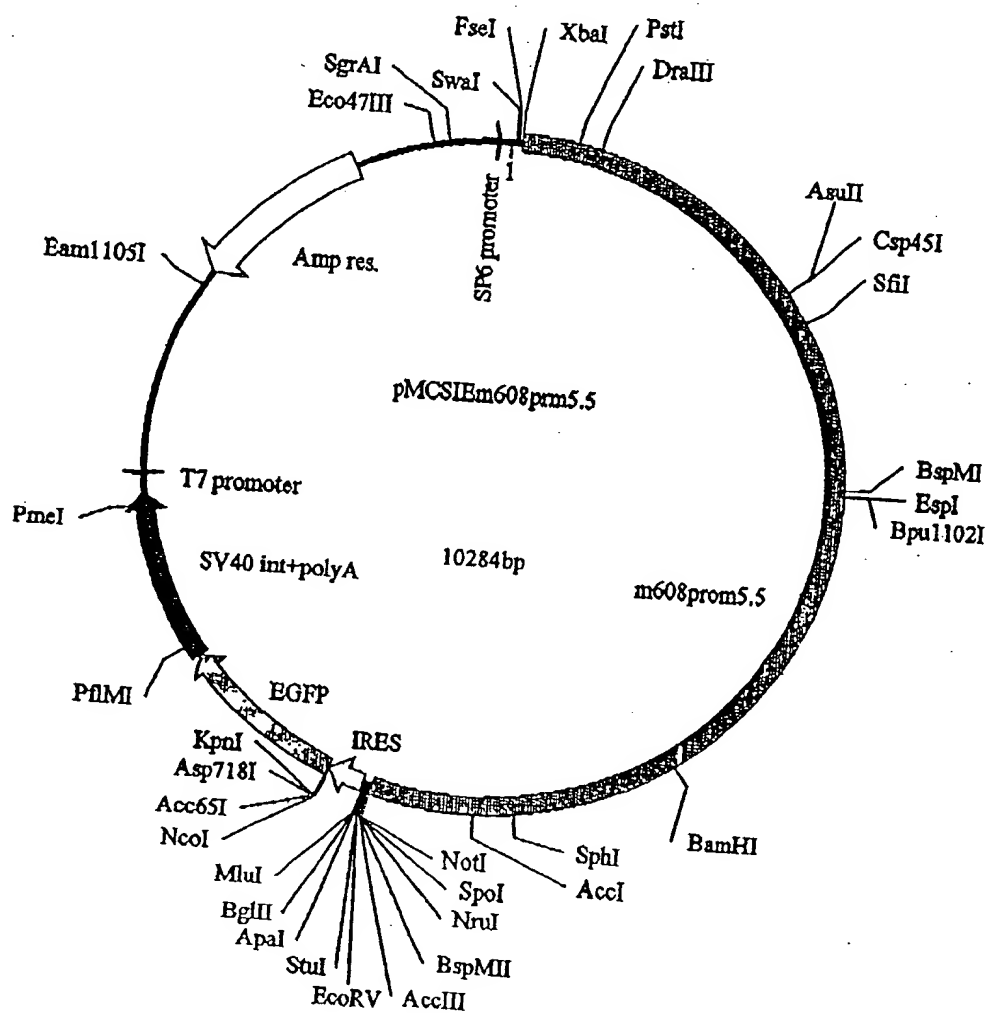


Figure 47

↓ (XbaI)

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Exon1

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↓ (BamHI)

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Figure 49

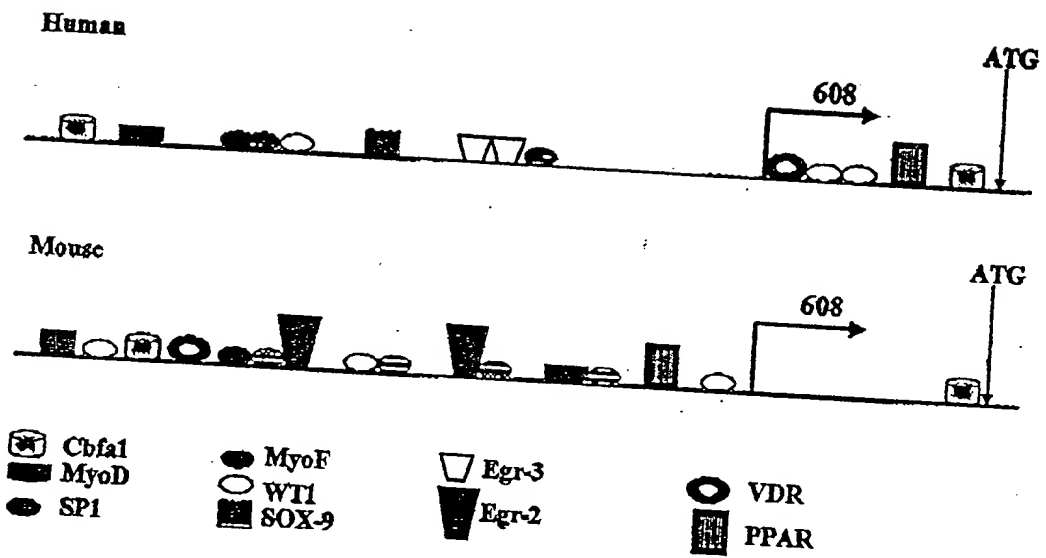


Figure 50

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GCTCCGCTTGGTACATCTAGAAGGAAACCGGCTGACAAAGCTCCATCCAGACACAT
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[illegible]

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[illegible]

Figure 52

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[illegible]

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 GCAAGCAATGGTTCCTTTATCATTTCTAAACAACCTCGGGAGGATGCAGGAAAATAT
 CGCTGTGCAGCTAGGAATAAAGTTGGCTATATTGAGAAATTAGTCATATTAGAAATT
 GGCCAGAAGCCAGTTATTCTTACCTATGCACCAGGGACAGTAAAAGGCATCAGTGGA
 GAATCTCTATCACTGCATTGTGTGTCTGATGGAATCCCTAAGCCAAATATCAAATGG
 ACTATGCCAAGTGGTTATGTAGTAGACAGGCCTCAAATTAATGGGAAATACATATTG
 CATGACAATGGCACCTTAGTCATTAAAGAAGCAACAGCTTATGACAGAGGAACTAT
 ATCTGTAAGGCTCAAAAATAGTGTTGGTCATACACTGATTACTGTTCCAGTAATGATT
 GTAGCCTACCCTCCCCGAATTACAAATCGTCCACCCAGGAGTATTGTCACCAGGACA
 GGGGCAGCCTTTCAGCTCCACTGTGTGGCCTTGGGAGTTCCCAAGCCAGAAATCACA
 TGGGAGATGCCTGACCACTCCCTTCTCTCAACGGCAAGTAAAGAGAGGACACATGGA
 AGTGAGCAGCTTCACTTACAAGGTACCCTAGTCATTGAGAATCCCCAAACCTCCGAT
 TCTGGGATATACAAATGCACAGCAAAGAACCCACTTGGTAGTGATTATGCAGCAACG
 TATATTCAAGTAATCTGA

Figure 54 Human OCP: predicted amino acid sequence

MKVKGRGITC LLVSFAVICL VATPGGKACP RRCACYMPTE VHCTFRYLTS
 IPDSIPPNVE RINLGYNSLV RLMETDFSGL TKLELLMLHS NGIHTIPDKT
 FSDLQALQVL KMSYNKVRKL QKDTFYGLRS LTRLHMDHNN IEFINPEVFY
 GLNFLRLVHL EGNQLTKLHP DTFVSLSYLQ IFKISFIKFL YLSDNFLTSL
 PQEMVSYMPD LDSLYLHGNP WTCDCHLKWL SDWIQEKPDV IKCKKDRSPS
 SAQQCPLCMN PRTSKGKPLA MVSAAAFQCA KPTIDSSLKS KSLTILEDSS
 SAFISPQGFN APFGSLTLNM TDQSGNEANM VCSIQKPSRT SPIAFTEEND
 YIVLNTSFST FLVCNIDYGH IQPVWQILAL YSDSPLILER SHLLSETPQL
 YYKYKQVAPK PEDIFTNIEA DLRADPSWLM QDQISLQLNR TATTFSTLQI
 QYSSDAQITL PRAEMRPVKH KWTMISRDNM TKLEHTVLVG GTVGLNCPGQ
 GDPTPHVDWL LADGSKVRAP YVSEDGRILI DKSGKLELQM ADSFDTGVYH
 CISSNYDDAD ILTYRITVVE PLVEAYQENG IHHTVFIGET LDLPCHSTGI
 PDASISWVIP GNNVLYQSSR DKKVLNNGTL RILQVTPKDQ GYYRCVAANP
 SGVDFLIFQV SVKMKGQRPL EHDGETEGSG LDESNPIAHL KEPPGAQLRT
 SALMEAEVGK HTSSTSKRHN YRELTQLRRG DSTHRRFREN RRHFPPSARR
 IDPQHWAAALL EKAKKNAMPD KRENTTVSPP PVVTQLPNIP GEEDDSSGML
 ALHEEFMVPA TKALNLPART VTADSRTISD SPMTNINYG T EFSPVVNSQI
 LPPEEPTDFK LSTAIKTTAM SKNINPTMSS QIQGTTNQHS STVFPLLLGA
 TEFQDSQDMG RGREHFQSRP PITVRTMIKD VNVKMLSSTT NKLLLESVNT
 TNSHQTSVRE VSEPRHNHFY SHTTQILSTS TFPSPHTAA HSQFPPIRNS
 TVNIPLFRRF GRQRKIGGRG RIISPYRTPV LRRHRSIFR STTRGSSEKS
 TTAFSATVLN VTCLSLCPRE RLTTATAALS FPSAAPITFP KADIARVPSE
 ESTTLVQNPL LLENKPSVE KTTPTIKYFR TEISQVTPTG AVMTYAPTST
 PMEKTHKVNA SYPRVSSTNE AKRDSVITSS LSGAITKPPM TIIAITRFSR
 RKIPWQQNFV NNHNPKGRLR NQHKVSLQKS TAVMLPKTSP ALPQRQSSPF
 HFTTLSTSVM QIPSNTLTTA HHTTTKTHNP GSLPTKKELP FPPLNPMPLPS
 IISKDSSTKS IISTQTAIPA TTPTFPASVI TYETQTERS AQTIQREQEP
 QKKNRTDPNI SPDQSSGFTT PTAMTPPALA FTHSPPENTT GISSTISFHS
 RTLNLTDVIE ELAQASTQTL KSTIASSETTL SSKSHQSTTT RKASLDTPIP
 PFLSSSATLM PVPISPPFTQ RAVTDTRGDS HFRLMTNTVV KLHESSRHLN
 QMPSSQLEPL TSSTSNLLHS TPMPALT TVK SQNSKLTPSP WAEYQFWHKP
 YSDIAEKGGK PEVSMLATTG LSEATTLVSD WDGQKNTKKS DFDKKPVQEA
 TTSKLLPFDS LSRYIFEKPR IVGGKAASFT IPANSDAFLP CEAVGNPLPT
 IHWTRVSGLD LSRGNQNSRV QVLPNGTSLI QRVEIQDRGQ YLCSASNLF
 TDHLHVTLSV VSYPPRILER RTKEITVHSG STVELKCRAE GRPSPTVTWI
 LANQTVVSES SQGSRQAVVT VDGTLLVHLN SIYDRGFYKC VASNPGGQDS
 LLVKIQVIAA PPVILEQRRQ VIVGTWGESL KLPCTAKGTP QPSVYVWLSD
 GTEVKPLQFT NSKLFLFSNG TLYIRNLASS DRGTYECIAT SSTGSERRVV
 MLTMEERVTS PRIEASQKR TEVNFGDKLL LNCSATGEPK PQIMWRLPSK
 AVVDQWSWIH VYPNGSLFIG SVTEKDSGVY LCVARNKMGD DLILMHVSLR
 LKPAKIDHKQ YFRKQVLHGK DFQVDCKASG SPVPEISWSL PDGTMINNAM
 QADDSGHRTR RYTLFNNGTL YFNKVGVAEE GDYTCYAQNT LGKDEMKVHL
 TVITAAPRIR QSNKTNKRIK AGDTAVLDCE VTGDPKPKIF WLLPSNDMIS
 FSIDRYTFHA NGSLTINKVK LLDSGEYVCV ARNPSGDDTK MYKLDVVSKP
 PLINGLYTNR TVIKATAVRH SKKHFDCAE GTPSPEVMWI MPDNIFLTAP
 YYGSRITVHK NGTLEIRNVR LSDSADFICV ARNEGGSVL VVQLEVLEML
 RRPTFRNPEN EKIVAQLGKS TALNCSVDGN PPPEIIWILP NGTRFSNGPQ
 SYQYLIASNG SFIISKTTRE DAGKYRCAAR NKVGYIEKLV ILEIGQKPMI



IGKYT

LTYAPGTVKG ISGESLSLHC VSDGIPKPN I KWTMPSGYV DRPQINGKYI
 LHDNGTLVIK EATAYDRGNY ICKAQN SVGH TLITVPVMIV AYP PRITNRP
 PRSIVTRTGA AFQLHCVALG VPKPEITWEM PDHSL LSTAS KER THGSEQL
 HLQGT LVIQN PQTS DSGIYK CTAKNPLGSD YAATYIQVI*

[illegible]